FIGURE 1

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

```
Primer HS-1     CGTGGCCATCCTGGGCAACACCCTG
                     G C GG         CT
                                    G
                                    T
```

HTRHR	CCTGGGCATTGTAGGCAACATCATGGT
HUMRANTES	CATTGGCCTGGTTGGAAACATCCTGGT
HSBLR1A	CCTGGGCGTGATCGGCAACGTCCTGGT
HUMSOMAT	GGTGGGGCTGGTGGGCAACGCCCTGGT
RNU02083	AGTGGGCCTCTTCGGAAACTTCCTGGT
U00442	GGTGGGCTTAGTGGGCAATTCCCTGGT
HUMNMBR	CGTGGGCTTGCTGGGCAACATCATGCT
HSHM4	GGTGACCATCATCGGCAACATCCTGGT
RATAADRE01	CTTTGCCATCGTGGGCAACATCTTGGT
HUMSSTR3X	GGTGGGCCTGCTGGGTAACTCGCTGGT
HUMC5AAR	GGTGGGAGTGCTGGGCAATGCCCTGGT
HUMRDC1A	CATCGGCATGATTGCCAACTCCGTGGT
HUMOPIODRE	CGTGGCGGTGCTCGGCAACCTCGTGGT
RATA2BAR	GCTGGCAGTGGCGGGCAACGTGCTGGT

FIGURE 2

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 3' SIDE PRIMER

Complementary Sequence to Primer HS-2	TTTGCCATCTGCTGGATGCCCCACAAC
	C C TTT C
	G G
	T T
HUMSGIR	TTTGCCCTCTGCTGGTTCCCTCTCAAC
HUMBOMB3S	TTTGCCCTCTGCTGGTTGCCAAATCAC
S46950	TTTGCCCTCTGCTGGCTGCCCCTACAC
MUSGPCR	TTTGCCCTCGTCTGGTGCCCTCTCAAC
S43387	TTTGCCCTTTTATGGATGCCCTACAGG
RATNEURA	TTTGCCATCTGCTGGCTGCCCTATCAC
RATA1ARA	TTTGCCCTCAGCTGGCTGCCGCTGCAT
HUMOPIODRE	TTTGCCATCTGCTGGCTGCCCTATCAC
HUMNEKAR	TTTGCCATCTGCTGGCTGCCCTACCAC
RATADENREC	TTTGCCTTGTGCTGGCTGCCTTTGTCC
HUMSRI1A	TTTGTCATCTGCTGGATGCCTTTCTAC
S8637154	TTTGCTATCTGCTGGCTGCCCTATCAT
RNCGPCR	TTTGCCGCCTGCTGGATGCCTTTTACC
HUMSSTR4Z	TTTGTGCTCTGCTGGATGCCTTTCTAC
RATGNRHA	TTTGCACACTGGTCGAAGCCAGACAAA

FIGURE 3

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer 3A

```
CTGACCGCTCTIACIACTGACCGATAC
     T T    GG GT    A C
                       G
```

Primer 3B

```
CTGACCGCTCTIACIACTGACCGATAT
     T T    GG GT    A C
                       G
```

L11064	CTCACCATGATGAGCGTGGACCGCTAC
L11065	TTGACCATGATGGAGTGTGACCGCTAC
D16349	CTCTGCACCATGAGCGTGGACCGCTAC
X69676	CTGATGCTCGTGAGTATCGACCGCTAC
M35328	CTTACGGCACTGTCAGCTGACAGGTAC
M73482	CTCACTGCCCTCAGCGCCGACAGGTAC
M73481	CTCACGGCGCTCTCGGCAGACAGATAC
L08893	TTAACAATTCTCAGCGCTGACAGATAC
X62933	ATGACCGCCATCGCCGCTGACAGGTAC
X62934	ATGACAACTGTGGCCTTTGACAGATAC
J05189	ATGACAGCCATTGCAGTGGACAGGTAT
M60786	CTCTGCGCTCTCAGTGTGGACAGGTAC
L04672	CTCACCTGCCTCAGCATTGACCGCTAC
X61496	TTGCTGGCTATCACTGTGGACCGCTAC
X59249	TTGCTGGCCATTGCTGTAGACCGATAC
L09249	CTCACCTGCCTCAGCATTGACCGCTAC
P30731	CTGACAGCTATCGCAGTGGACCGCCAC
M31210	CTCCTCGCCATCGCCATTGAGCGCTAT
U03642	CTCACCGGCCTCAGCTTCGACCGCTAC

FIGURE 4

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

```
Primer 3C         CTCGCCGCTATIAGCATGGACCGITAC
                       G  CC  G T     T

Primer 3D         CTCGCCGCTATIAGCATGGACCGITAT
                       G  CC  G T     T


L32840            ATTACCTGCATGAGTGTCGATAGGTAC
X64052            CTCACGTGTCTCAGCATCGATCGCTAC
M90065            CTCACGTGTCTCAGCATCGATCGCTAC
M91464            CTCACGTGTCTCAGCATTGATCGATAC
M88096            CTGGTAGCCATCTCTCTGGAGAGATAT
M99418            CTCGTGGCCATAGCCCTGGAGCGATAC
L04473            CTCGTGGCCATCGCACTGGAGCGGTAC
M73969            CTGGCCTGCATCAGTGTGGACCGTTAC
X65858            TTGGCCTGCATCAGTGTGGACCGTTAC
S46665            CTGGCTACCATTAGTGCCGACCGTTTC
M60626            ATCGCCCTCATTGCTCTGGACCGCTGT
```

FIGURE 5

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 3' SIDE PRIMER

Complementary Sequence to Primer 6A	TTTACCITCTGTTGGICGCCCTACCACATC GT TC T T
Complementary Sequence to Primer 6B	TTCACCITCTGTTGGICGCCCTACCACATC GT TC T T

L11064	TTCGTGGTGTGCTGGGCGCCCATCCACATC
L11065	TTCATCATCTGTTGGACCCCCATTCACATC
D16349	TTTATCGTCTGCTGGACCCCCATCCACATC
X69676	TTTGTGCTGTGTTGGGTGCCTTTCCAGATC
M35328	TTTGCCTTCTGCTGGCTCCCCAACCATGTC
M73482	TTCATCTTCTGTTGGTTTCCAAACCACATC
M73481	TTCGCCTTCTGCTGGCTCCCCAATCATGTC
L08893	TTTGCCCTCTGCTGGTTGCCAAATCACCTC
X62933	TTTGCCATCTGCTGGCTGCCCTACCACCTC
X62934	TTCGCCATCTGCTGGCTGCCCTTCCACATC
J05189	TTTGCCATCTGCTGGCTGCCCTATCACGTG
M60786	TTCGCCCTGTGCTGGTTCCCTCTTCACTTA
L04672	TTTGTCATCTGCTGGCTGCCCTACCACGTG
X61496	TTTGCCGCCTGCTGGATGCCTTTTACCCTC
X59249	TTTGCCTTGTGCTGGCTGCCTTTGTCCATC
L09249	TTTGCCATCTGCTGGCTGCCCTACCACGTG
P30731	TTTGCCCTCTGCTGGTTCCCTCTCAACTGC
M31210	TTCATCGCCTGCTGGGCACCGCTCTTCATC
U03642	TTTGCCCTGTGCTGGATGCCCTACCACCTG

FIGURE 6

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 3' SIDE PRIMER

```
Complementary Sequence   TTTTTCITTTGCTGGITTCCCTACCACATG
to Primer 6C               CC T  G C          T T
```

L32840	TTCATCATTTGCTGGCTTCCCTTCCATGTT
X64052	TTCTTCTTTTCCTGGGTTCCCCACCAAATA
M90065	TTCTTCTTTTCCTGGGTTCCCCACCAAATA
M91464	TTTTTCTTTTCCTGGATTCCCCACCAAATA
M88096	TTCTTCCTGTGCTGGATGCCCATCTTCAGC
M99418	TTCTTCCTGTGTTGGCTGCCAGTGTACAGC
L04473	TTTTTTCTGTGTTGGTTGCCAGTTTATAGT
M73969	TTCCTGCTTTGCTGGCTGCCCTACAACCTG
X65858	TTCCTGCTTTGCTGGCTGCCCTACAACCTG
S46665	TTCTTTATCTTCTGGCTGCCCTATCAGGTG
M60626	TTTTTTCTCTGCTGGTCCCCATATCAGGTG

FIGURE 7

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

```
Primer T2A          GTCACCAACITGTTCATCCTCAICCTG
                     C        AC        GT T
                                           A
```

HUMGALAREC	ACCACCAACCTGTTCATCCTCAACCTG
RATADRA1B	CCCACCAACTACTTTATCGTCAACCTG
HUMADRB1	ACCACCAACCTGTTCATCCTCAACCTG
RABIL8RSB	GTCACCGACGTCTACCTGCTGAACCTG
HUMOPIODRE	GTCACCAACTCCTTCCTCGTGAACCTG
BTSKR	GTGACCAACTACTTCATCGTCAACCTG
HUMSRI2A	ATCACCAACATTTACATCCTCAACCTG
HUMSSTR3Y	GTCACCAACGTCTACATCCTCAACCTG
HUMGARE	GTCACCAACGCCTTCCTCCTCTCACTG
HUMCCKAR	GTCACCAACATCTTCCTCCTCTCCCTG
HUMSHTR	CCCTCCAACTACCTGATCGTGTCCCTG
HUMD1B	ATGACCAACGTCTTCATCGTGTCTCTG
HUM5HT1E	CCTGCCAACTACCTAATCTGTTCTCTG
HUMD4C	CCCACCAACTCCTTCATCGTGAGCCTG
MMSERO	GCCACCAACTATTTCCTGATGTCACTT
RATADRA1A	GTCACCAACTATTTCATCGTGAACCTG
S57565	CTGACCAATTGCTTCATTGTGTCCCTG

FIGURE 8

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence to Primer T7A	AACCCCITCITCTATTGCTTTITCICT T T C C C G G
HUMGALAREC	AATCCTATCATTTATGCATTTCTCTCT
RATA1ADREC	AACCCCATCGTCTATGCCTTCCGGATC
PIGA2R	AATCCTCTCTTTTATGGCTTTCTGGGG
RAT5HTRTC	AACCCTATCATCTACCCGCTCTTTATG
S58541	AACCCCATCATTTATGCCTTTAATGCT
HUMGRPR	AACCCCTTTGCCCTCTACCTGCTGAGC
MUSGRPBOM	AACCCCTTTGCTCTTTATCTGCTGAGC
RRVT1AIIR	AACCCTCTGTTCTACGGCTTTCTGGGG
HUMADRB1	AACCCCATCATCTACTGCCGCAGCCCC
HSHM4	AACCCCGTGTGCTATGCTCTGTGCAAC
HUMGARE	AACCCCCTGGTCTACTGCTTCATGCAC
RATCCKAR	AACCCCATCATCTATTGCTTCATGAAC
S59749	AATCCCATGCTCTACACCTTCGCTGGC
HUMSST28A	AACCCCGTCCTCTACGGCTTCCTCTCG
RNGPROCR	AACCCCATCCTCTACGGCTTCCTCTCC
MUSSSRI1A	AACCCCATACTCTACGGCTTCCTGTCG
HUMA1AADR	AACCCGCTCATCTACCCCTGTTCCAGC
S66181	AACCCGGTTCTCTACGCCTTCCTGGAC
HUMSSTR3Y	AACCCCATCCTTTATGGCTTCCTCTCC

FIGURE 9

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

```
Primer TM1-A2       TGITGGTTATIGGIGTTGTIGGIAA
                        CC GC    C   G
```

MUSBB2R	TGGTGGTGGTGGTGGTGGTGGGCAA
BTSKR	TGGTGCTGGTGGCTGTGATGGGCAA
BOVEETBR	TGTTCGTGCTGGGCATCATCGGAAA
HUMNEUYREC	TGATCATTCTTGGTGTCTCTGGAAA
MMSUBKREC	TGGTGCTGGTGGCTGTAACAGGCAA
HUMPGE2R	TGTTCATCTTCGGGGTGGTGGGCAA
HUMPIR	TGTTCGTGGCCGGTGTGGTGGGCAA
HSU11053	TGTTCGTCGTGGGCTTGGTGGGCAA
RRMC3RA	TGGTGATCCTGGCTGTGGTGAGGAA
HUMMR	TGGTTATCCTGGCCGTGGTCAGGAA
MUSGRPBOM	TCATCGTGATAGGTCTTATTGGCAA
RATCHOLREC	TCTTTCTGATGAGTGTTGGCGGAAA
RATCCKAR	TATTCCTTCTCAGTGTGCGGGGGAA

FIGURE 10

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence to Primer TM3-B2	GCCATIACCITGGACAGATACCGAT A T A C G A G
HUMCCKR	GCCATCGCACTGGAGCGGTACAG
HUMCCKBGR	GCCATCGCACTGGAGCGGTACAG
MMGMC5R	GCCATTGCGGTGGACAGGTACA
HUMV2R	GCCATGACGCTGGACCGCCACCG
RATNEURA	GCCATTGCAGTGGACAGGTA
DOGGSTRN	GCCATCGCCCTGGAGCGATACAG
RAT5HT5A	GCAATAGCTTTGGACCGCTACTGGT
MUSALP2ADA	GCCATTAGTCTGGACCGCTACTGGT
HUMADORA1X	GCAATTGCTGTGGACCGCTACC
HUMOPIODRE	GCCATCGCGGTGGACAGATACA
MUSGRPBOM	GCACTGTCAGCTGACAGGTACAAA
RATCCKAR	GCCATCTCTCTGGAGAGATATGG
HSTRHREC	GCCTTTACCATTGAGAGGTACATA

FIGURE 11

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

```
Primer TM3-C2          CATGGCCGTGGAGAGITACITGGC
                         TT  C    C     T  A
```

HUMNK3R	CATTGCGGTGGACAGGTATATGGC
HSMRNAOXY	CATGTCCCTGGACCGCTGCCTGGC
S68242	CATATCGCTGGAGAGATACGGAGC
CFGPCR4	CATCGCTCTGGACAGGTACTGGGC
MMSUBPREC	TGGCCTTTGACAGATACATGGC
HUMOPIODRE	CATCGCGGTGGACAGATACATGGC
HUMGALAREC	ATGTCCGTGGACCGCTACGTGGC
HSS31G	CATTGCCCTGGACAGGTACTGGGC
HUMARB3A	CCTGGCCGTGGACCGCTACCTGGC
HUMHPR	CATGGCCGTGGAGCGCTGCCTGGC
RATCCKAR	CATCTCTCTGGAGAGATATGGCGC

FIGURE 12

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

```
Complementary Sequence   TTTGCCITCTGCTGGATCCCCAAC
to Primer TM6-E2           C     G       C G   TT
```

HUMNEKAR	TTTGCCATCTGCTGGCTGCCCTAC
HUMSUBPRA	TTCGCCATCTGCTGGCTGCCCTTC
RATSKR	TTTGCCATCTGCTGGCTGCCCTAC
MUSGRPBOM	TTTGCCTTCTGCTGGCTCCCCAAC
HUMOPIODRE	TTTGCCATCTGCTGGCTGCCCTA
HUMA2XXX	TTTGCCCTCTGCTGGCTGCCCCT
HUMADRBR	TTCACCCTCTGCTGGCTGCCCTTC
CFGPCR8	TTCGCCCCTCTGTGGCTGCCCCT
HUMETSR	TTTGCCCTCTGCTGGCTTCCCCT
MMNPY1CDS	TTCGCCGTCTGCTGGCTGCCCCT
HSMRNAOXY	TTCATCGTGTGCTGGACGCCTTTC
RATCCKAR	TTCTTCCTGTGCTGGATGCCCATC

FIGURE 13

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer TM2F18	ARYYTIGCIITIGCNGAY
HUMTSHX	AACCTGGCCTTTGCGGAT
HUMNEKAR	AATCTGGCGCTGGCTGAC
HUMFMLP	AACCTGGCCGTGGCTGAC
HUMINTLEU8	AACCTAGCCTTGGCCGAC
HUMA1AADR	AACCTGGCCGTGGCCGAC
HUMIL8RA	AACCTGGCCTTGGCCGAC
HSDD2	AGCCTCGCAGTGGCCGAC
HUMANTIR	AATTTAGCACTGGCTGAC
HUMSOMAT	AACCTGGCCGTAGCCGAC
HUMEL4REC	AGCTTGGCTGTGGCTGAT
HSTRHREC	AGCCTGGCAGTAGCTGAT
HSU07882	AACCTGGCCTTAGCCGAT

(R = A or G, Y = C or T, N = A, C, G or T, and I = Inosine)

FIGURE 14

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence to Primer TM6R21	TTYNYNNTNTGYTGGITICCI
HSBAR	TTCACCCTCTGCTGGCTGCCC
HUMNEKAR	TTTGCCATCTGCTGGCTGCCC
HUMETN1R	TTTGCTCTTTGCTGGTTCCCT
HUMHISH2R	TTCATCATCTGCTGGTTTCCC
HUMA1AADR	TTCGTGCTCTGCTGGTTCCCT
HUMIL8RA	TTCCTGCTTTGCTGGCTGCCC
HUMNMBR	TTCATCTTCTGTTGGTTTCCT
HUMNKIRX	TTCGCCATCTGCTGGCTGCCC
HUMSUBPRA	TTCGCCATCTGCTGGCTGCCC
HUM5HT1DA	TTTATCATCTGCTGGCTGCCC
HUMPFPR2A	TTCTTCATCTGTTGGTTTCCC
HSDD2	TTCATCATCTGCTGGCTGCCC
HUMNEUYREC	TTTGCAGTCTGCTGGCTCCCT
HUM2XXX	TTTGCCCTCTGCTGGCTGCCC
HUMBK2A	TTCATCATCTGCTGGCTGCCC
HUMFMLPX	TTCTTCATCTGTTGGTTTCCC
HUMSSTR3X	TTCGTGCTCTGCTGGATGCCC
HUMCCKR	TTTTTTCTGTGTTGGTTGCCA
HSNEURA	TTTGTGGTCTGCTGGCTGCCC

(Y = C or T, N = A, C, G or T, and I = Inosine)

FIGURE 15

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer S3A	GCCTGITIAIGATGAGTGTGGAIAGIT
	C G C TC C
HUMGALAREC	CCCTGGCCGCGATGTCCGTGGACCGCT
S70057	GCCTCGTGGCCATCGCACTGGAGCGGT
S67127	ACCTCTGCGCTCTTAGTGTTGACAGGT
S44866	GTCTATGTGCTCTGAGTATTGACAGAT
HUMC5AAR	TCCTGGCCACCATCAGCGCCGACCGCT
HUMANTIR	TACTCACGTGTCTCAGCATTGATCGAT
HUMBK2A	TCCTGATGCTGGTGAGCATCGACCGCT
HSNEURA	ACGTGGCCAGCCTGAGTGTGGAGCGCT
HUMGRPR	CACTCACGGCGCTCTCGGCAGACAGAT
HUMFSRS	GCCTGACAGTCATGAGCGTGGACCGCT
HUMIL8RA	TGTTGGCCTGCATCAGTGTGGACCGTT
HUMNEKAR	CCATGACCGCCATTGCTGCCGACAGGT

FIGURE 16

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence to Primer S6A	TGGITICCCTACCACITIATCAICATC T T GG GT
HUMGALAREC	TGGCTGCCGCACCACATCATCCATCTC
S70057	TGGTTGCCAGTTTATAGTGCCAACACG
S67127	TGGTTCCCTCTTCATTTAAGCCGTATA
S44866	TGGCTTCCCCTTCACCTCAGCAGGATT
HUMC5AAR	TGGTTGCCCTACCAGGTGACGGGGATA
HUMANTIR	TGGATTCCCCACCAAATATTCACTTTT
HUMBK2A	TGGCTGCCCTTCCAGATCAGCACCTTC
HSNEURA	TGGACTCCGTTCCTCTATGACTTCTAC
HUMGRPR	TGGCTCCCCAATCATGTCATCTACCTG
HUMFSRS	TGGCTGCCCTTCTTCACCGTCAACATC
HUMIL8RA	TGGCTGCCCTACAACCTGGTCCTGCTG
HUMNEKAR	TGGCTGCCCTACCACCTCTACTTCATC

FIGURE 17

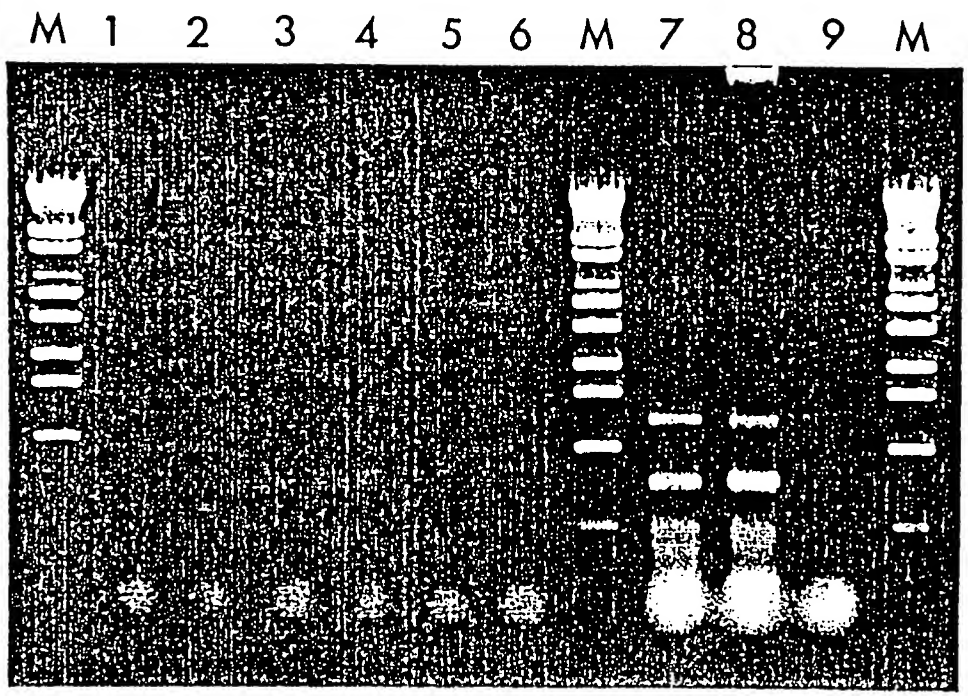
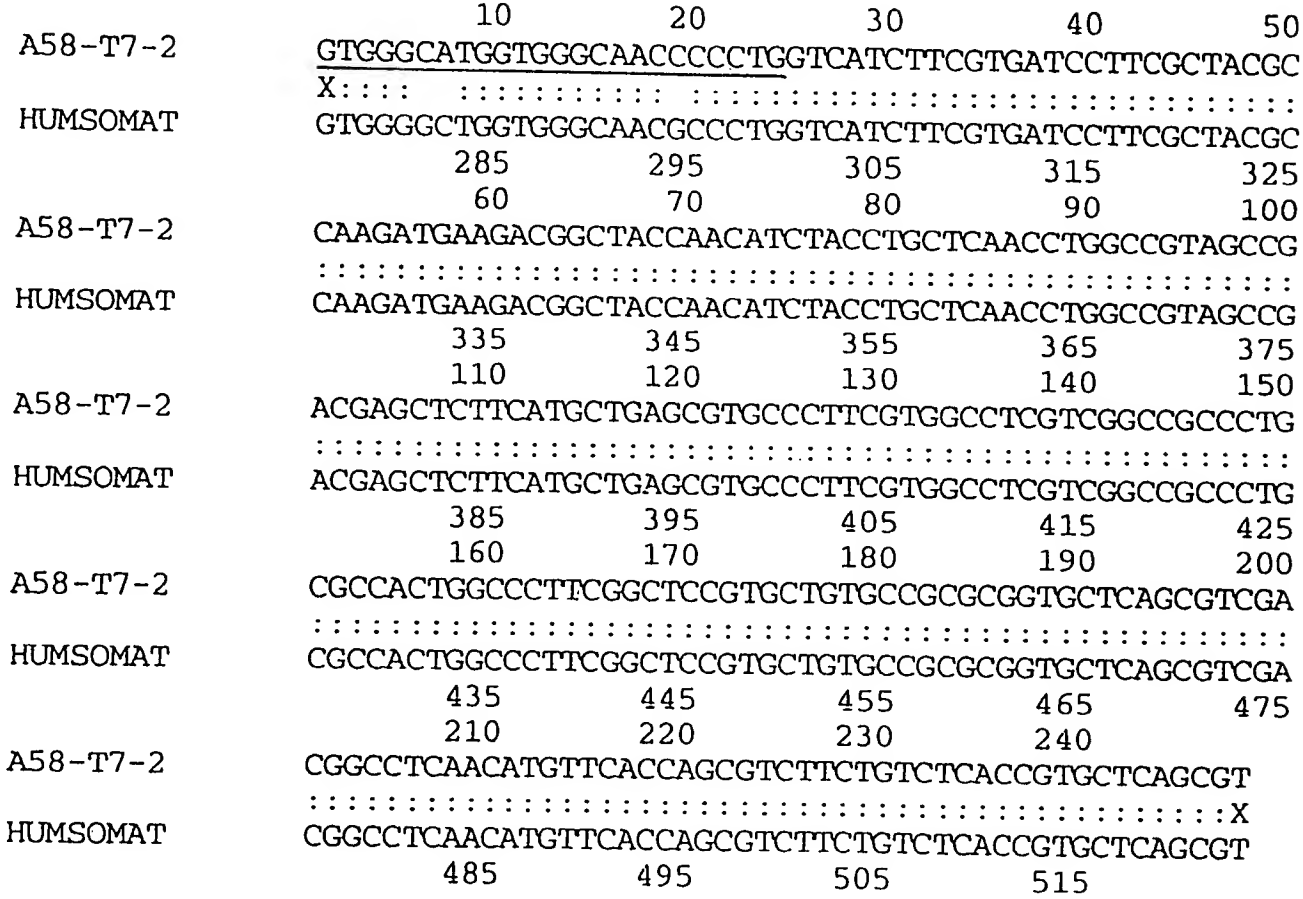


FIGURE 18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A58-T7-2 GTGGGCATGGTGGGCAACCCCCTGGTCATCTTCGTGATCCTTCGCTACGC
X:::: :::::::::: ::::::::::::::::::::::::::::::
HUMSOMAT GTGGGGCTGGTGGGCAACGCCCTGGTCATCTTCGTGATCCTTCGCTACGC
285 295 305 315 325
60 70 80 90 100
A58-T7-2 CAAGATGAAGACGGCTACCAACATCTACCTGCTCAACCTGGCCGTAGCCG
::
HUMSOMAT CAAGATGAAGACGGCTACCAACATCTACCTGCTCAACCTGGCCGTAGCCG
335 345 355 365 375
110 120 130 140 150
A58-T7-2 ACGAGCTCTTCATGCTGAGCGTGCCCTTCGTGGCCTCGTCGGCCGCCCTG
::
HUMSOMAT ACGAGCTCTTCATGCTGAGCGTGCCCTTCGTGGCCTCGTCGGCCGCCCTG
385 395 405 415 425
160 170 180 190 200
A58-T7-2 CGCCACTGGCCCTTCGGCTCCGTGCTGTGCCGCGCGGTGCTCAGCGTCGA
::
HUMSOMAT CGCCACTGGCCCTTCGGCTCCGTGCTGTGCCGCGCGGTGCTCAGCGTCGA
435 445 455 465 475
210 220 230 240
A58-T7-2 CGGCCTCAACATGTTCACCAGCGTCTTCTGTCTCACCGTGCTCAGCGT
::X
HUMSOMAT CGGCCTCAACATGTTCACCAGCGTCTTCTGTCTCACCGTGCTCAGCGT
485 495 505 515

FIGURE 19

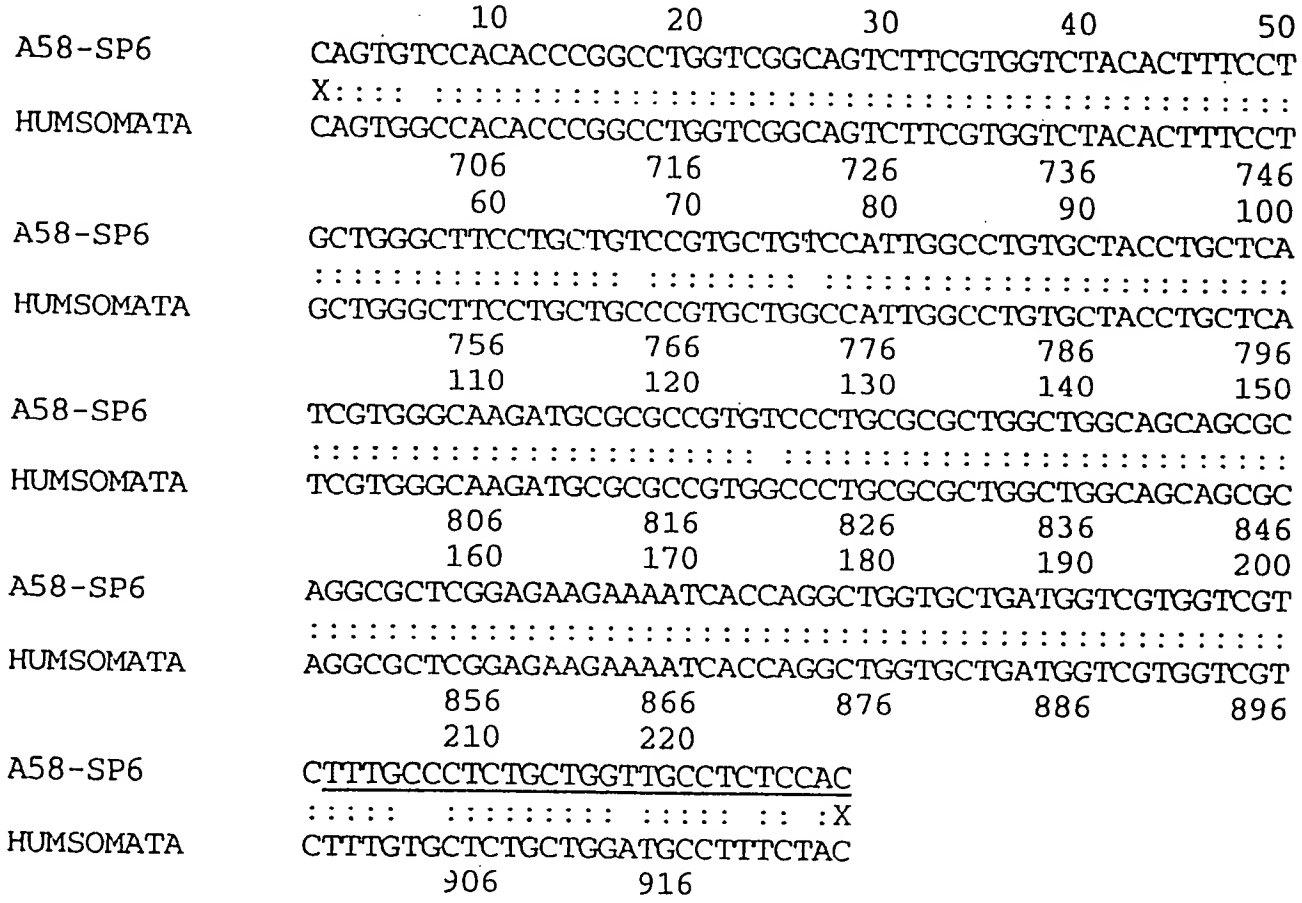

10 20 30 40 50
A58-SP6
CAGTGTCCACACCCGGCCTGGTCGGCAGTCTTCGTGGTCTACACTTTCCT
X:::: ::
HUMSOMATA
CAGTGGCCACACCCGGCCTGGTCGGCAGTCTTCGTGGTCTACACTTTCCT
706 716 726 736 746
60 70 80 90 100
A58-SP6
GCTGGGCTTCCTGCTGTCCGTGCTGTCCATTGGCCTGTGCTACCTGCTCA
::::::::::::::: :::::::: ::::::::::::::::::::::::
HUMSOMATA
GCTGGGCTTCCTGCTGCCCGTGCTGGCCATTGGCCTGTGCTACCTGCTCA
756 766 776 786 796
110 120 130 140 150
A58-SP6
TCGTGGGCAAGATGCGCGCCGTGTCCCTGCGCGCTGGCTGGCAGCAGCGC
:::::::::::::::::::::::: ::::::::::::::::::::::::
HUMSOMATA
TCGTGGGCAAGATGCGCGCCGTGGCCCTGCGCGCTGGCTGGCAGCAGCGC
806 816 826 836 846
160 170 180 190 200
A58-SP6
AGGCGCTCGGAGAAGAAAATCACCAGGCTGGTGCTGATGGTCGTGGTCGT
::
HUMSOMATA
AGGCGCTCGGAGAAGAAAATCACCAGGCTGGTGCTGATGGTCGTGGTCGT
856 866 876 886 896
210 220
A58-SP6
CTTTGCCCTCTGCTGGTTGCCTCTCCAC
::::: ::::::::: ::::: :: :X
HUMSOMATA
CTTTGTGCTCTGCTGGATGCCTTTCTAC
906 916

FIGURE 20

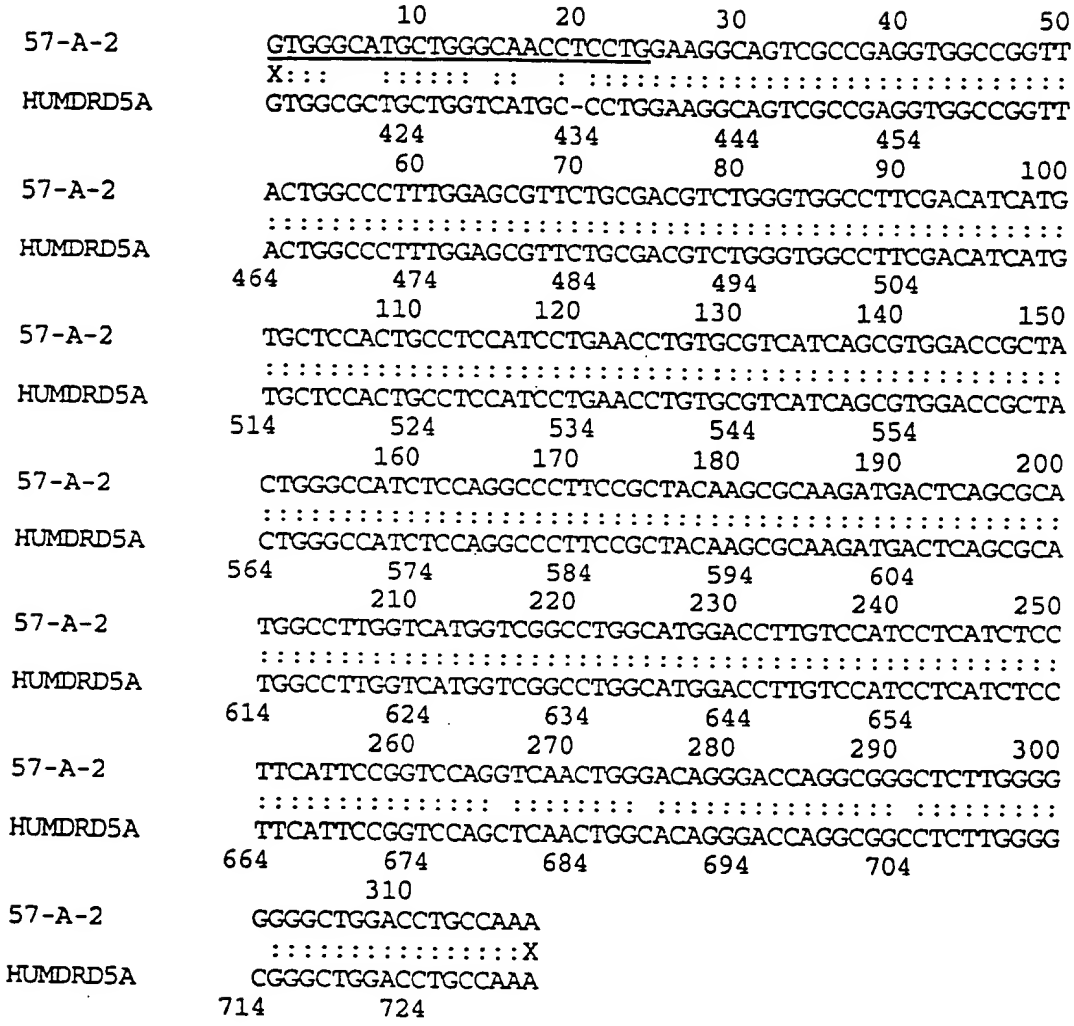
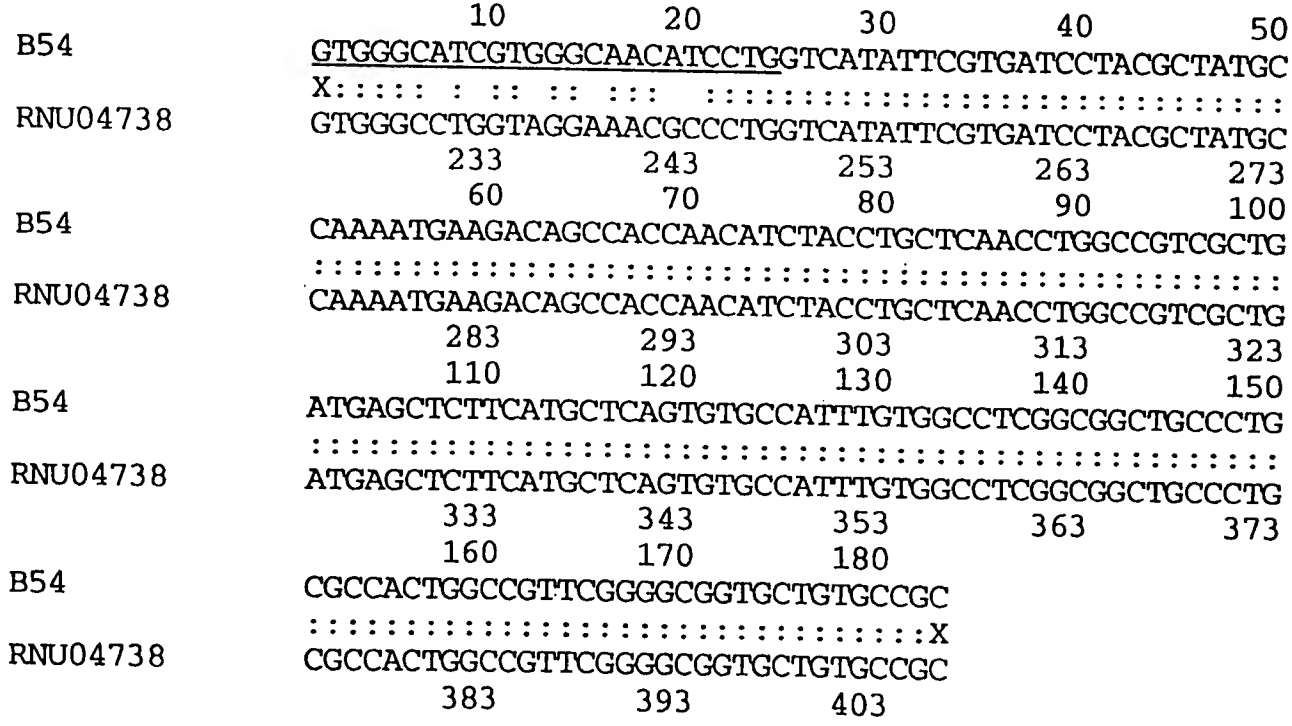


FIGURE 21


10 20 30 40 50
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RNU04738 GTGGGCCTGGTAGGAAACGCCCTGGTCATATTCGTGATCCTACGCTATGC
233 243 253 263 273
60 70 80 90 100
B54 CAAAATGAAGACAGCCACCAACATCTACCTGCTCAACCTGGCCGTCGCTG
RNU04738 CAAAATGAAGACAGCCACCAACATCTACCTGCTCAACCTGGCCGTCGCTG
283 293 303 313 323
110 120 130 140 150
B54 ATGAGCTCTTCATGCTCAGTGTGCCATTTGTGGCCTCGGCGGCTGCCCTG
RNU04738 ATGAGCTCTTCATGCTCAGTGTGCCATTTGTGGCCTCGGCGGCTGCCCTG
333 343 353 363 373
160 170 180
B54 CGCCACTGGCCGTTCGGGGCGGTGCTGTGCCGC
RNU04738 CGCCACTGGCCGTTCGGGGCGGTGCTGTGCCGC
383 393 403

FIGURE 22

```
                9          18          27          36          45          54
5'  GTG GGC ATG GTG GGC AAC GTC CTG CTG GTG CTG GTG ATC GCG CGG GTG CGC CGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val Arg Arg

               63          72          81          90          99         108
    CTG CAC AAC GTG ACG AAC TTC CTC ATC GGC AAC CTG GCC TTG TCC GAC GTG CTC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu

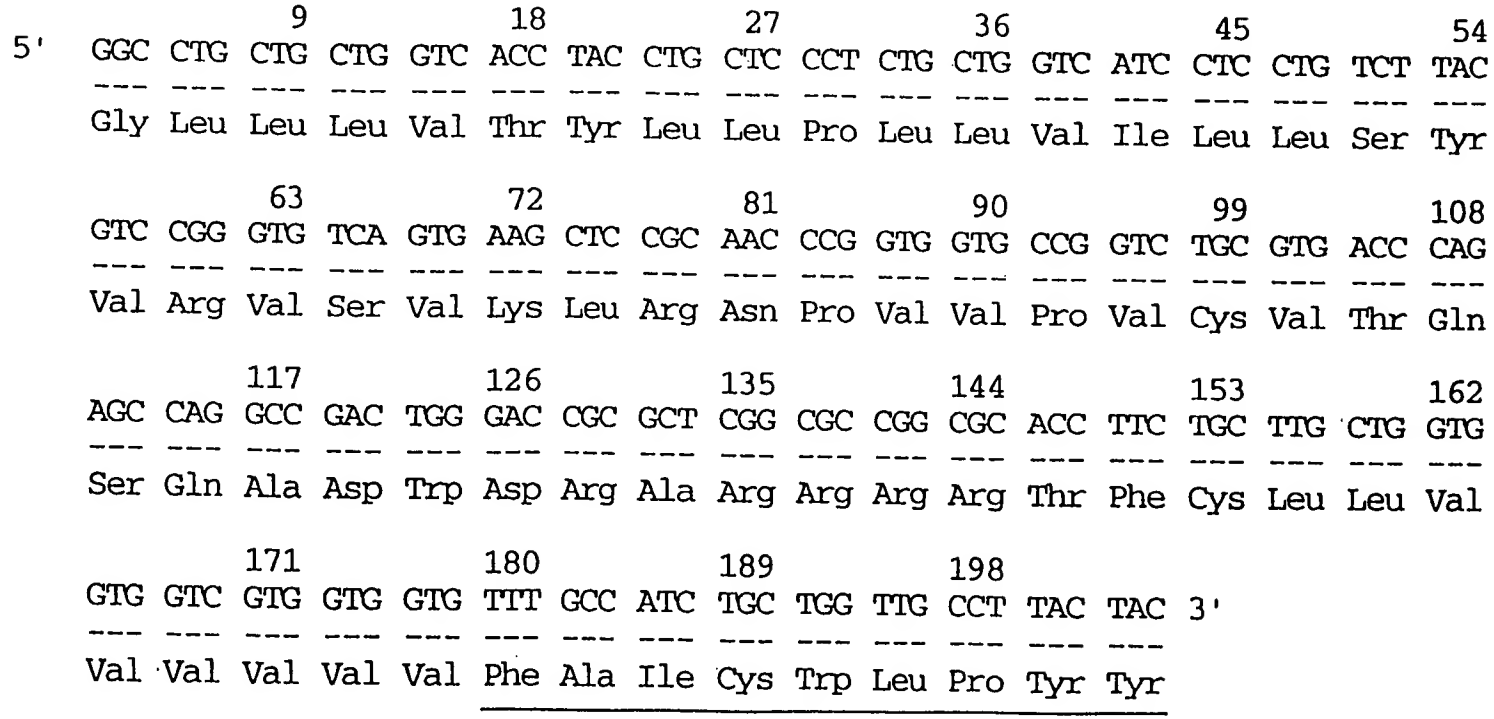
              117         126         135         144         153         162
    ATG TGC ACC GCC TGC GTG CCG CTC ACG CTG GCC TAT GCC TTC GAG CCA CGC GGC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly

              171         180         189         198         207         216
    TGG GTG TTC GGC GGC GGC CTG TGC CAC CTG GTC TTC TTC CTG CAG CCG GTC ACC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Trp Val Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr

              225         234         243         252         261         270
    GTC TAT GTG TCG GTG TTC ACG CTC ACC ACC ATC GAA GTG GAC CGG TAC GTC GGT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Glu Val Asp Arg Tyr Val Gly

              279         288         297
    GCT GGT GCA CCC GCT GAG GCG GGG CAT 3'
    --- --- --- --- --- --- --- --- ---
    Ala Gly Ala Pro Ala Glu Ala Gly His
```

FIGURE 23


5'
9 18 27 36 45 54
GGC CTG CTG CTG GTC ACC TAC CTG CTC CCT CTG CTG GTC ATC CTC CTG TCT TAC
Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr
63 72 81 90 99 108
GTC CGG GTG TCA GTG AAG CTC CGC AAC CCG GTG GTG CCG GTC TGC GTG ACC CAG
Val Arg Val Ser Val Lys Leu Arg Asn Pro Val Val Pro Val Cys Val Thr Gln
117 126 135 144 153 162
AGC CAG GCC GAC TGG GAC CGC GCT CGG CGC CGG CGC ACC TTC TGC TTG CTG GTG
Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu Val
171 180 189 198
GTG GTC GTG GTG GTG TTT GCC ATC TGC TGG TTG CCT TAC TAC 3'
Val Val Val Val Val Phe Ala Ile Cys Trp Leu Pro Tyr Tyr

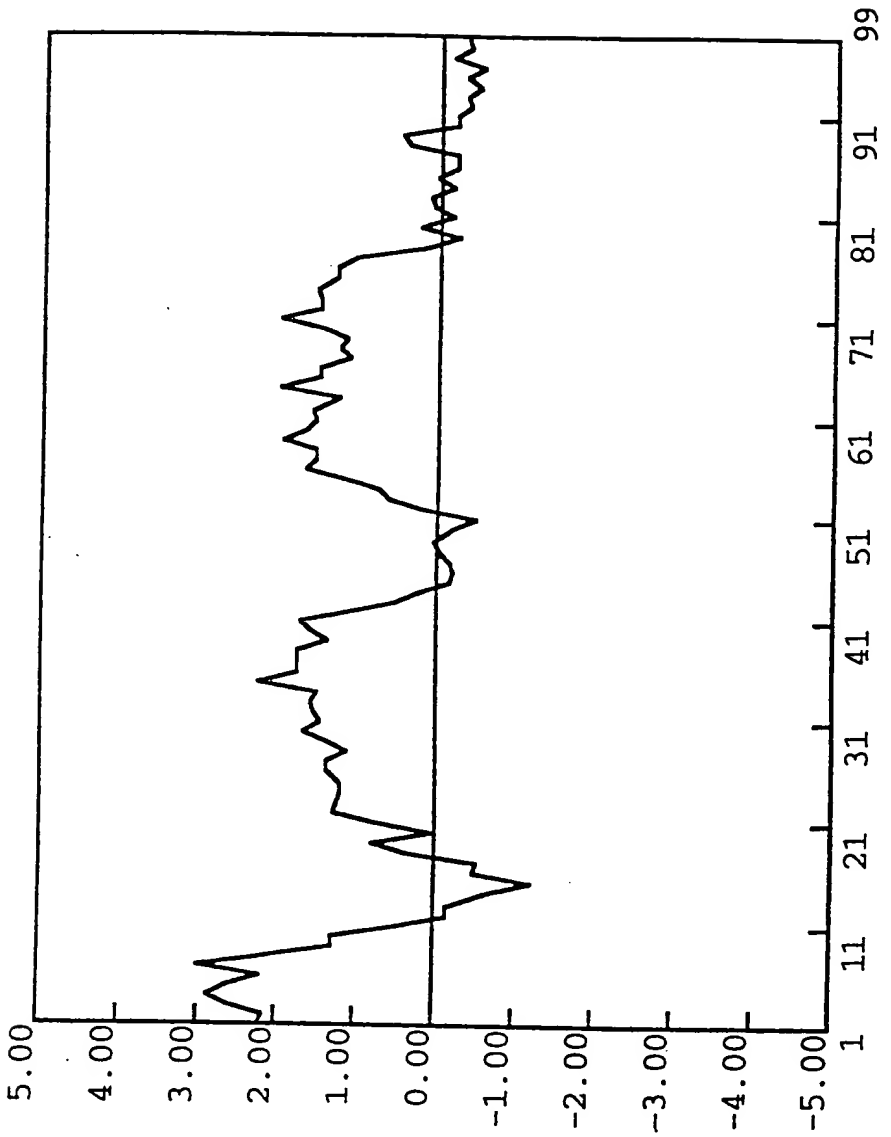


FIGURE 24

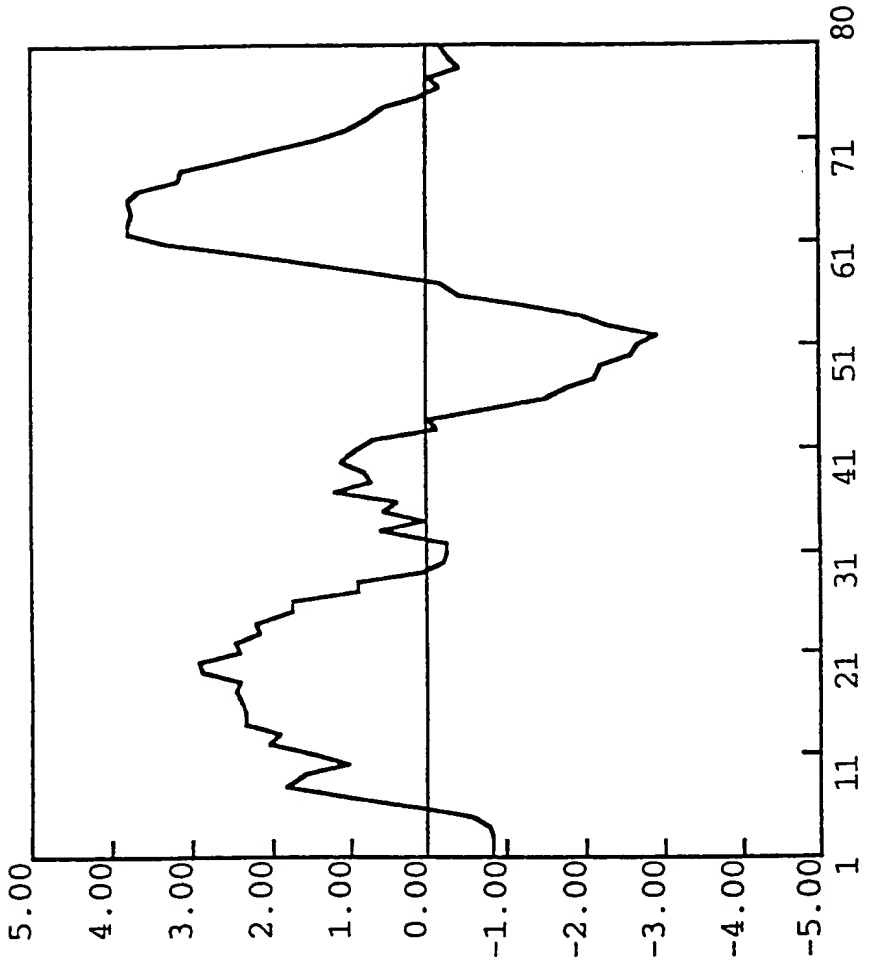


FIGURE 25

FIGURE 26

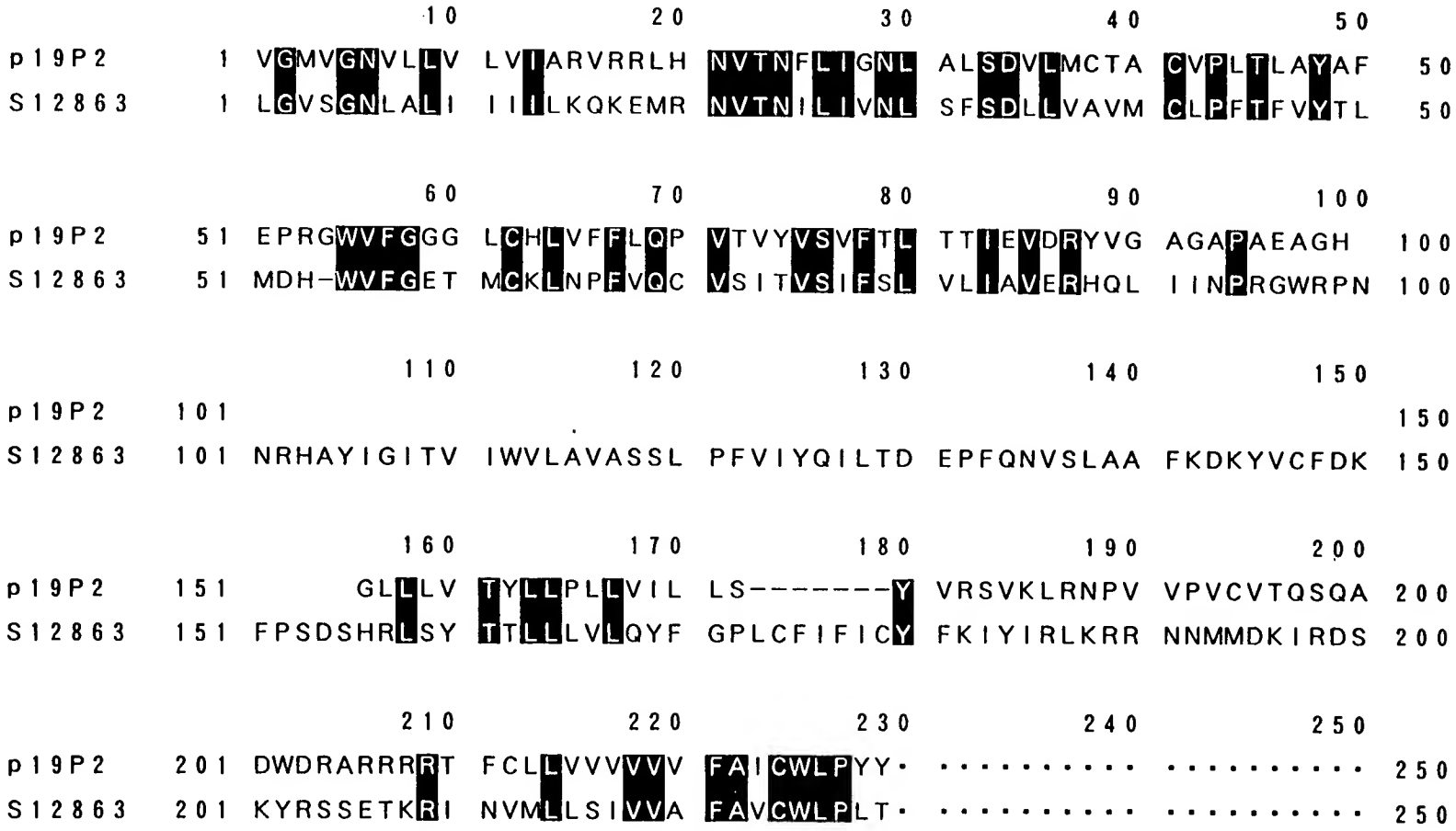

10 20 30 40 50
p19P2 1 VGMVGNVLLV LVIARVRRLH NVTNFLIGNL ALSDVLMCTA CVPLTLAYAF 50
S12863 1 LGVSGNLALI IIILKQKEMR NVTNILIVNL SFSDLLVAVM CLPFTFVYTL 50
60 70 80 90 100
p19P2 51 EPRGWVFGGG LCHLVFFLQP VTVYVSVFTL TTIEVDRYVG AGAPAEAGH 100
S12863 51 MDH-WVFGET MCKLNPFVQC VSITVSIFSL VLIAVERHQL IINPRGWRPN 100
110 120 130 140 150
p19P2 101 150
S12863 101 NRHAYIGITV IWVLAVASSL PFVIYQILTD EPFQNVSLAA FKDKYVCFDK 150
160 170 180 190 200
p19P2 151 GLLLV TYLLPLLVIL LS--------Y VRSVKLRNPV VPVCVTQSQA 200
S12863 151 FPSDSHRLSY TTLLLVLQYF GPLCFIFICY FKIYIRLKRR NNMMDKIRDS 200
210 220 230 240 250
p19P2 201 DWDRARRRRT FCLLVVVVVV FAICWLPYY· ·····
S12863 201 KYRSSETKRI NVMLLSIVVA FAVCWLPLT· ·····

FIGURE 27

```
                9                 18                27                36                45                54
5' GTG GGC ATG GTG GGC AAC ATC CTG CTG GTG CTG GTG ATC GCG CGG GTG CGC CGG
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Val Gly Met Val Gly Asn Ile Leu Leu Val Leu Val Ile Ala Arg Val Arg Arg

                63                72                81                90                99               108
   CTG TAC AAC GTG ACG AAT TTC CTC ATC GGC AAC CTG GCC TTG TCC GAC GTG CTC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Leu Tyr Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu

               117               126               135               144               153               162
   ATG TGC ACC GCC TGC GTG CCG CTC ACG CTG GCC TAT GCC TTC GAG CCA CGC GGC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly

               171               180               189               198               207               216
   TGG GTG TTC GGC GGC GGC CTG TGC CAC CTG GTC TTC TTC CTG CAG GCG GTC ACC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Trp Val Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Ala Val Thr

               225               234               243               252               261               270
   GTC TAT GTG TCG GTG TTC ACG CTC ACC ACC ATC GCA GTG GAC CGC TAC GTC GTG
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr Val Val

               279               288               297               306               315               324
   CTG GTG CAC CCG CTG AGG CGG CGC ATC TCG CTG CGC CTC AGC GCC TAC GCT GTG
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val

               333               342               351               360               369               378
   CTG GCC ATC TGG GTG CTG TCC GCG GTG CTG GCG CTG CCC GCC GCC GTG CAC ACC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Leu Ala Ile Trp Val Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr

               387               396               405               414               423               432
   TAT CAC GTG GAG CTC AAG CCG CAC GAC GTG CGC CTC TGC GAG GAG TTC TGG GGC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Tyr His Val Glu Leu Lys Pro His Asp Val Arg Leu Cys Glu Glu Phe Trp Gly

               441               450               459               468               477               486
   TCC CAG GAG CGC CAG CGC CAG CTC TAC GCC TGG GGG CTG CTG CTG GTC ACC TAC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Ser Gln Glu Arg Gln Arg Gln Leu Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr

               495               504               513               522               531               540
   CTG CTC CCT CTG CTG GTC ATC CTC CTG TCT TAC GCC CGG GTG TCA GTG AAG CTC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu

               549               558               567               576               585               594
   CGC AAC CGC GTG GTG CCG GGC CGC GTG ACC CAG AGC CAG GCC GAC TGG GAC CGC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Arg Asn Arg Val Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg

               603               612               621               630               639               648
   GCT CGG CGC CGG CGC ACC TTC TGC TTG CTG GTG GTG GTC GTG GTG GTG TTC ACC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val Phe Thr

               657               666
   CTC TGC TGG CTG CCC TTC TTC 3'
   --- --- --- --- --- --- ---
   Leu Cys Trp Leu Pro Phe Phe
```

FIGURE 28

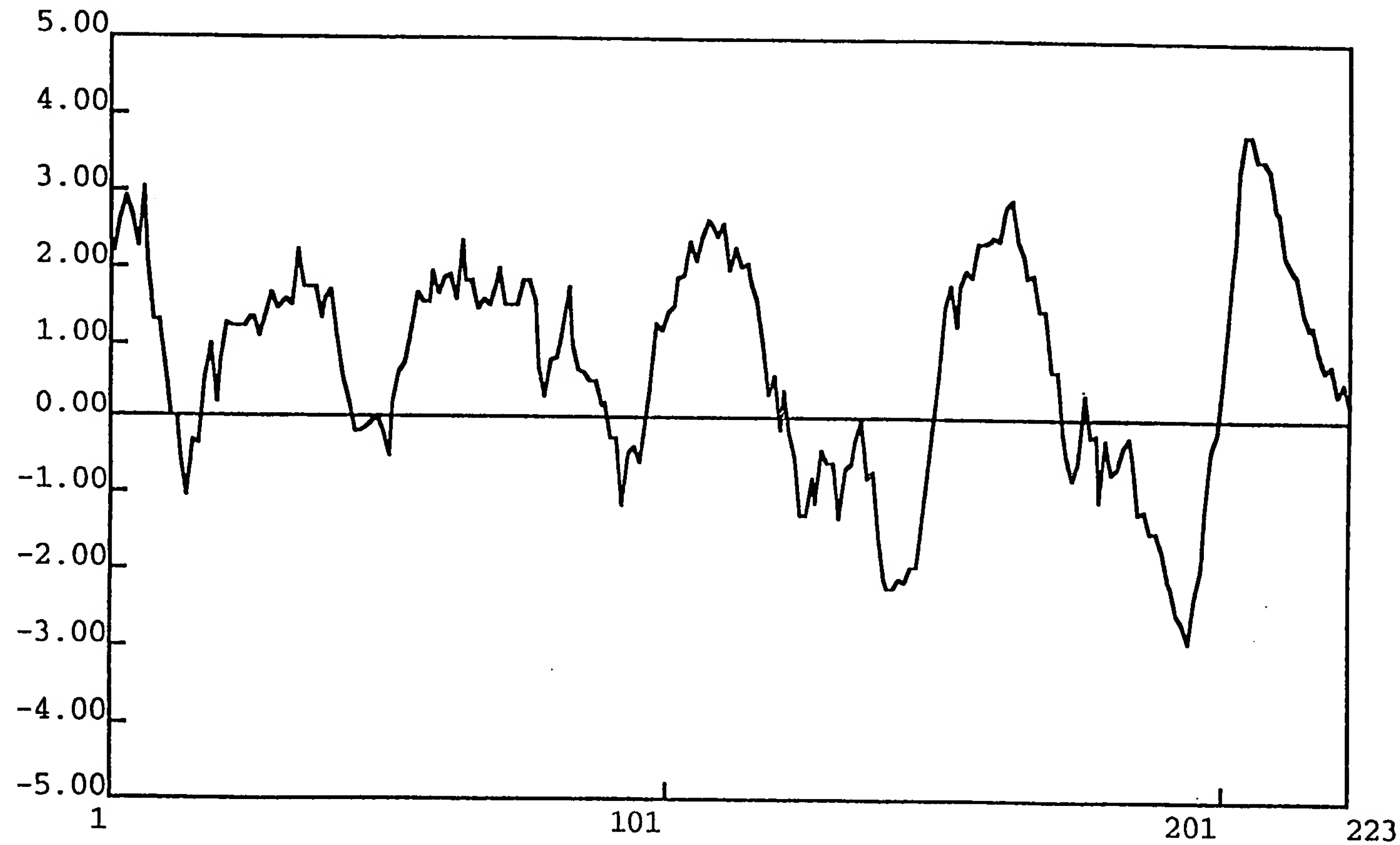


FIGURE 29

```
                10                  19                  28                  37                  46                  55
5'  GTG GGC ATG CTG GGC AAC GCC CTG GTC TGT CAT GTC ATC TTC AAG AAC CAG CGA
    ___________________________________ --- --- --- --- --- --- --- --- ---
                                        Val Cys His Val Ile Phe Lys Asn Gln Arg

                64                  73                  82                  91                  100                 109
    ATG CAC TCG GCC ACC AGC CTC TTC ATC GTC AAC CTG GCA GTT GCC GAC ATA ATG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Met His Ser Ala Thr Ser Leu Phe Ile Val Asn Leu Ala Val Ala Asp Ile Met

                118                 127                 136                 145                 154                 163
    ATC ACG CTG CTC AAC ACC CCC TTC ACT TTG GTT CGC TTT GTG AAC AGC ACA TGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ile Thr Leu Leu Asn Thr Pro Phe Thr Leu Val Arg Phe Val Asn Ser Thr Trp

                172                 181                 190                 199                 208                 217
    ATA TTT GGG AAG GGC ATG TGC CAT GTC AGC CGC TTT GCC CAG TAC TGC TCA CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ile Phe Gly Lys Gly Met Cys His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu

                226                 235
    CAC GTC TCA GCA CTG ACA 3'
    --- --- --- --- --- ---
    His Val Ser Ala Leu Thr
```

FIGURE 30

```
                9          18          27          36          45          54
5'  GAG CCA GCT GAC CTC TTC TGG AAG AAC CTG GAC TTG CCC ACC TTC ATC CTG CTC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Glu Pro Ala Asp Leu Phe Trp Lys Asn Leu Asp Leu Pro Thr Phe Ile Leu Leu

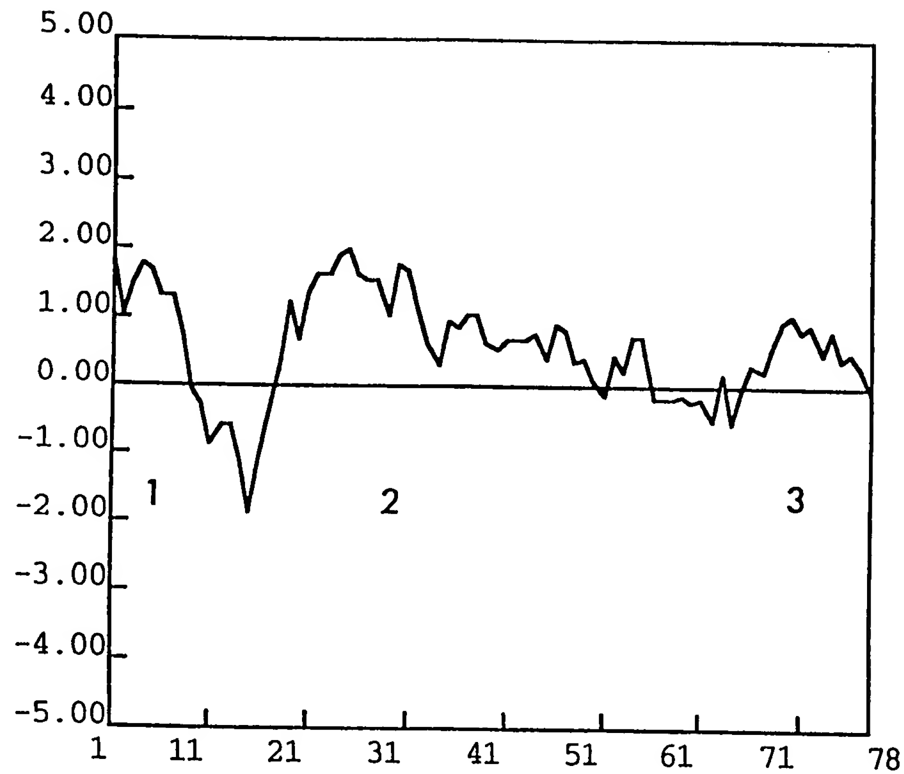
               63          72          81          90          99         108
    AAC ATC CTG CCC CTC CTC ATC ATC TCT GTG GCC TAC GTT CGT GTG ACC AAG AAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Asn Ile Leu Pro Leu Leu Ile Ile Ser Val Ala Tyr Val Arg Val Thr Lys Lys

              117         126         135         144         153         162
    CTG TGG CTG TGT AAT ATG ATT GTC GAT GTG ACC ACA GAG CAG TAC TTT GCC CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Leu Trp Leu Cys Asn Met Ile Val Asp Val Thr Thr Glu Gln Tyr Phe Ala Leu

              171         180         189         198         207         216
    CGG CCC AAA AAG AAG AAG ACC ATC AAG ATG TTG ATG CTG GTG GTA GTC CTC TTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Arg Pro Lys Lys Lys Lys Thr Ile Lys Met Leu Met Leu Val Val Val Leu Phe

              225         234
    GCC CTC TGC TGG TTG CCT CTC GAC 3'
    --- --- --- --- --- --- --- ---
    Ala Leu Cys Trp Leu Pro Leu Asp
```

FIGURE 31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4.00
3.00
2.00
1.00
0.00
-1.00
-2.00
-3.00
-4.00
-5.00
1
11
21
31
41
51
61
71
78
1
2
3

FIGURE 32

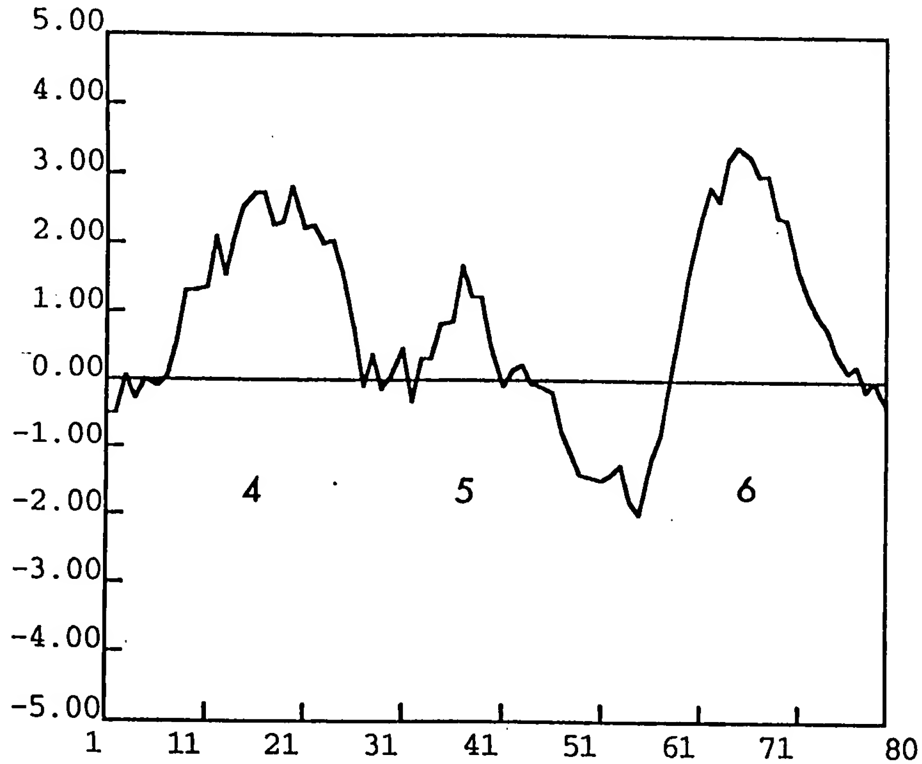


FIGURE 33

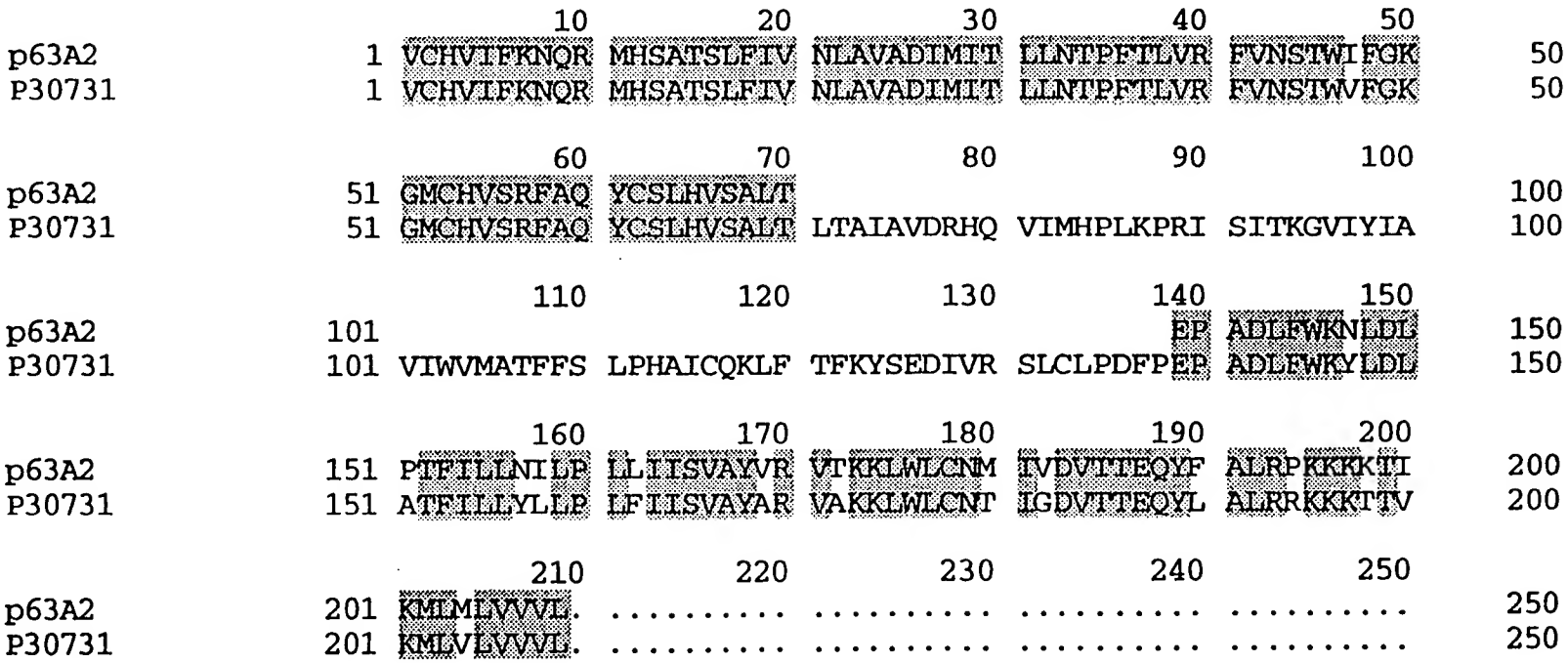


FIGURE 34

```
   1 CATCGTCAAGCAGATGAAGATCATCCACGAGGATGGCTACTCCGAGGGCCAGCAGAAATT   60
   1                                                                 1

  61 CTGCCCCTTCTTCCCGCGAGTGCTTTCCCGCTCTCCAAACCCCACTCCCAGGTGGCCATG  120
   1                                                          Met    1

 121 GCCTCATCGACCACTCGGGGCCCCAGGGTTTCTGACTTATTTTCTGGCTGCCGCCGGCG  180
   1 AlaSerSerThrThrArgGlyProArgValSerAspLeuPheSerGlyLeuProProAla   21

 181 GTCACAACTCCCGCCAACCAGAGCGCAGAGGCCTCGGCGGGCAACGGGTCGGTGGCTGGC  240
  21 ValThrThrProAlaAsnGlnSerAlaGluAlaSerAlaGlyAsnGlySerValAlaGly   41

 241 GCGGACGCTCCAGCCGTCACGCCCTTCCAGAGCCTGCAGCTGGTGCATCAGCTGAAGGGG  300
  41 AlaAspAlaProAlaValThrProPheGlnSerLeuGlnLeuValHisGlnLeuLysGly   61

 301 CTGATCGTGCTGCTCTACAGCGTCGTGGTGGTCGTGGGGCTGGTGGGCAACTGCCTGCTG  360
  61 LeuIleValLeuLeuTyrSerValValValValValGlyLeuValGlyAsnCysLeuLeu   81

 361 GTGCTGGTGATCGCGCGGGTGCGCCGGCTGCACAACGTGACGAACTTCCTCATCGGCAAC  420
  81 ValLeuValIleAlaArgValArgArgLeuHisAsnValThrAsnPheLeuIleGlyAsn  101

 421 CTGGCCTTGTCCGACGTGCTCATGTGCACCGCCTGCGTGCCGCTCACGCTGGCCTATGCC  480
 101 LeuAlaLeuSerAspValLeuMetCysThrAlaCysValProLeuThrLeuAlaTyrAla  121

 481 TTCGAGCCACGCGGCTGGGTGTTCGGCGGCGGCCTGTGCCACCTGGTCTTCTTCCTGCAG  540
 121 PheGluProArgGlyTrpValPheGlyGlyGlyLeuCysHisLeuValPhePheLeuGln  141

 541 CCGGTCACCGTCTATGTGTCGGTGTTCACGCTCACCACCATCGCAGTGGACCGCTACGTC  600
 141 ProValThrValTyrValSerValPheThrLeuThrThrIleAlaValAspArgTyrVal  161

 601 GTGCTGGTGCACCCGCTGAGGCGGCGCATCTCGCTGCGCCTCAGCGCCTACGCTGTGCTG  660
 161 ValLeuValHisProLeuArgArgArgIleSerLeuArgLeuSerAlaTyrAlaValLeu  181

 661 GCCATCTGGGCGCTGTCCGCGGTGCTGGCGCTGCCCGCCGCCGTGCACACCTATCACGTG  720
 181 AlaIleTrpAlaLeuSerAlaValLeuAlaLeuProAlaAlaValHisThrTyrHisVal  201

 721 GAGCTCAAGCCGCACGACGTGCGCCTCTGCGAGGAGTTCTGGGGCTCCCAGGAGCGCCAG  780
 201 GluLeuLysProHisAspValArgLeuCysGluGluPheTrpGlySerGlnGluArgGln  221

 781 CGCCAGCTCTACGCCTGGGGGCTGCTGCTGGTCACCTACCTGCTCCCTCTGCTGGTCATC  840
 221 ArgGlnLeuTyrAlaTrpGlyLeuLeuLeuValThrTyrLeuLeuProLeuLeuValIle  241

 841 CTCCTGTCTTACGTCCGGGTGTCAGTGAAGCTCCGCAACCGCGTGGTGCCGGGCTGCGTG  900
 241 LeuLeuSerTyrValArgValSerValLysLeuArgAsnArgValValProGlyCysVal  261

 901 ACCCAGAGCCAGGCCGACTGGGACCGCGCTCGGCGCCGGCGCACCTTCTGCTTGCTGGTG  960
 261 ThrGlnSerGlnAlaAspTrpAspArgAlaArgArgArgArgThrPheCysLeuLeuVal  281

 961 GTGGTCGTGGTGGTGTTCGCCGTCTGCTGGCTGCCGCTGCACGTCTTCAACCTGCTGCGG 1020
 281 ValValValValValPheAlaValCysTrpLeuProLeuHisValPheAsnLeuLeuArg  301

1021 GACCTCGACCCCCACGCCATCGACCCTTACGCCTTTGGGCTGGTGCAGCTGCTCTGCCAC 1080
 301 AspLeuAspProHisAlaIleAspProTyrAlaPheGlyLeuValGlnLeuLeuCysHis  321

1081 TGGCTCGCCATGAGTTCGGCCTGCTACAACCCCTTCATCTACGCCTGGCTGCACGACAGC 1140
 321 TrpLeuAlaMetSerSerAlaCysTyrAsnProPheIleTyrAlaTrpLeuHisAspSer  341

1141 TTCCGCGAGGAGCTGCGCAAACTGTTGGTCGCTTGGCCCCGCAAGATAGCCCCCCATGGC 1200
 341 PheArgGluGluLeuArgLysLeuLeuValAlaTrpProArgLysIleAlaProHisGly  361

1201 CAGAATATGACCGTCAGCGTGGTCATCTGATGCCACTTAGCCAGGCCTTGGTCAAGGAGC 1260
 361 GlnAsnMetThrValSerValValIle***                                371

1261 TCCACTTCAACTGGCCTCCTAGGGCACCACTCGAGGTCAATCTGGTGCTTATTCTCAGCA 1320
 371                                                               371

1321 CCAGAGCTAGC                                                  1331
 371                                                               371
```

FIGURE 35

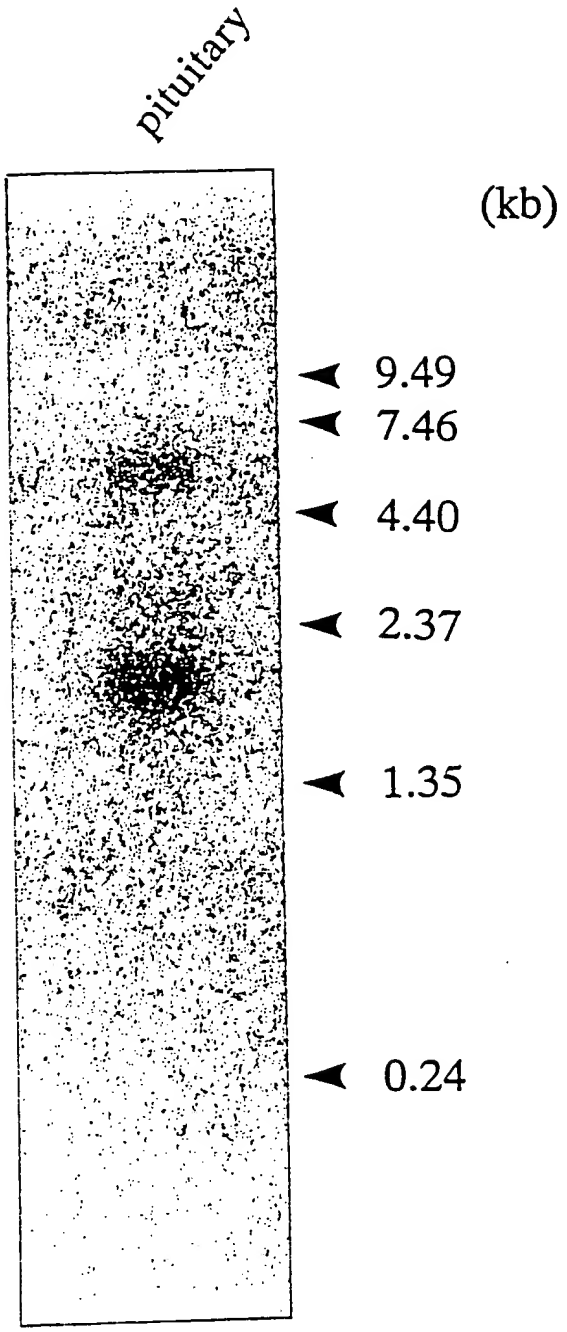
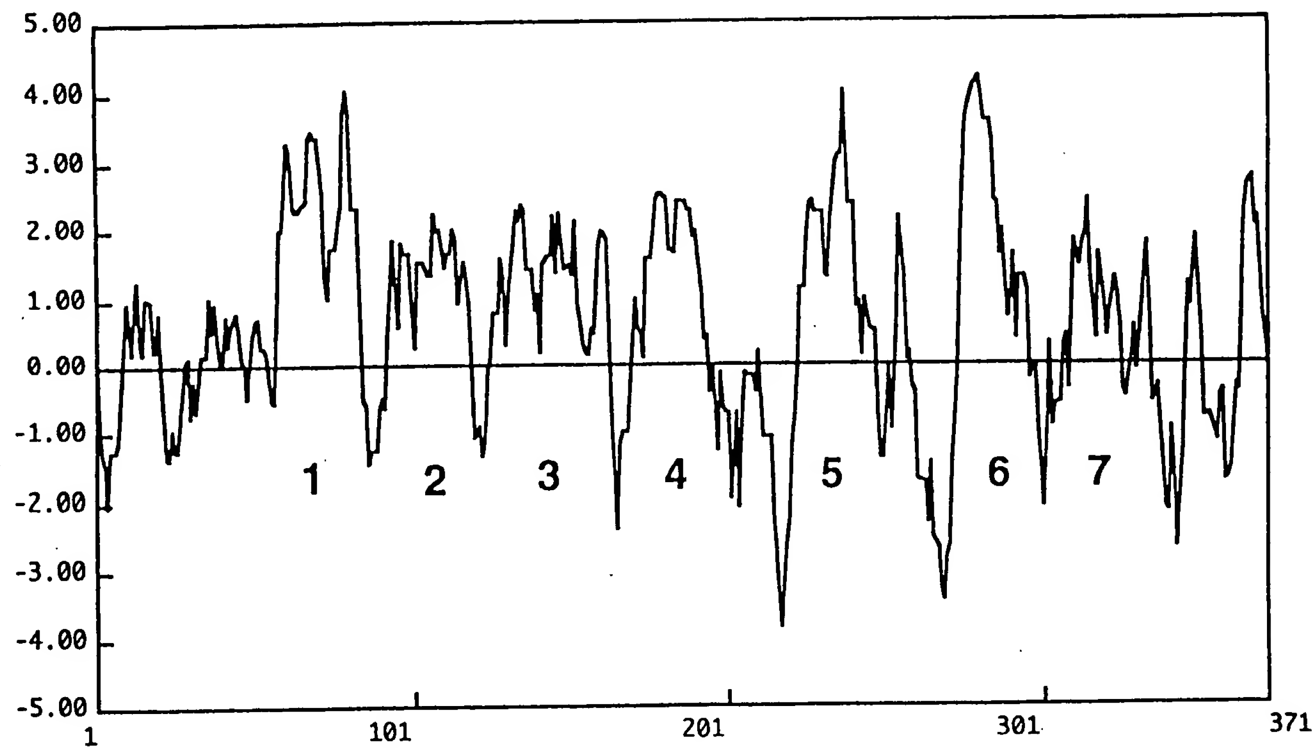


FIGURE 36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4.00
3.00
2.00
1.00
0.00
-1.00
-2.00
-3.00
-4.00
-5.00
1
101
201
301
371
1
2
3
4
5
6
7

FIGURE 37

```
             9             18            27            36            45            54
5' GTG GGC CTG GTG GGC AAC ATC CTG GCT TCC TGG CAC AAG CGT GGA GGT CGC CGT
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Val Gly Leu Val Gly Asn Ile Leu Ala Ser Trp His Lys Arg Gly Gly Arg Arg

            63            72            81            90            99           108
   GCT GCT TGG GTA GTG TGT GGA GTC GTG TGG CTG GCT GTG ACA GCC CAG TGC CTG
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Ala Ala Trp Val Val Cys Gly Val Val Trp Leu Ala Val Thr Ala Gln Cys Leu

           117           126           135           144           153           162
   CCC ACG GCA GTC TTT GCT GCC ACA GGC ATC CAG CGC AAC CGC ACT GTG TGC TAC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Pro Thr Ala Val Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val Cys Tyr

           171           180           189           198           207           216
   GAC CTG AGC CCA CCC ATC CTG TCT ACT CGC TAC CTG CCC TAT GGT ATG GCC CTC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Asp Leu Ser Pro Pro Ile Leu Ser Thr Arg Tyr Leu Pro Tyr Gly Met Ala Leu

           225           234           243           252           261           270
   ACG GTC ATC GGC TTC TTG CTG CCC TTC ATA GCC TTA CTG GCT TGT TAT TGT CGC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Thr Val Ile Gly Phe Leu Leu Pro Phe Ile Ala Leu Leu Ala Cys Tyr Cys Arg

           279           288           297           306           315           324
   ATG GCC CGC CGC CTG TGT CGC CAG GAT GGC CCA GCA GGT CCT GTG GCC CAA GAG
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Met Ala Arg Arg Leu Cys Arg Gln Asp Gly Pro Ala Gly Pro Val Ala Gln Glu

           333           342           351           360           369           378
   CGG CGC AGC AAG GCG GCT CGT ATG GCT GTG GTG GTG GCA GCT GTC TTT GCC CTC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Arg Arg Ser Lys Ala Ala Arg Met Ala Val Val Val Ala Ala Val Phe Ala Leu

           387           396
   TGC TGG CTG CCT CTC TAC 3'
   --- --- --- --- --- ---
   Cys Trp Leu Pro Leu Tyr
```

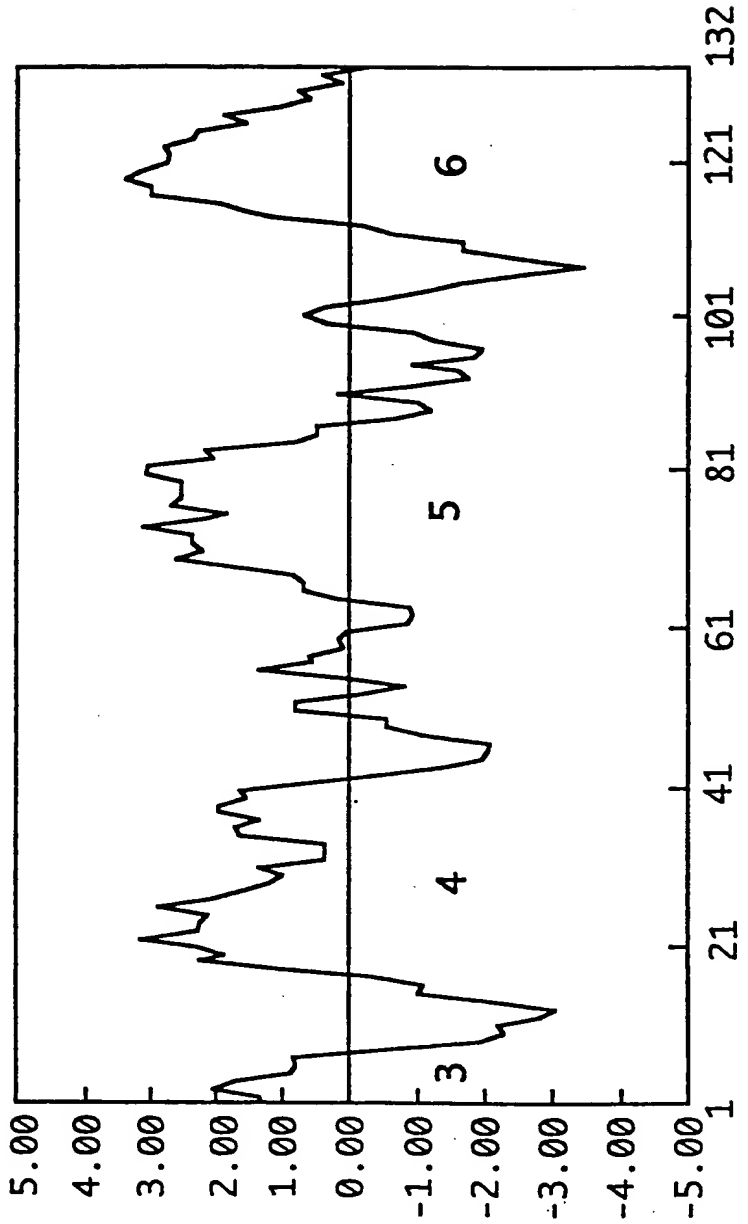


FIGURE 38

FIGURE 39

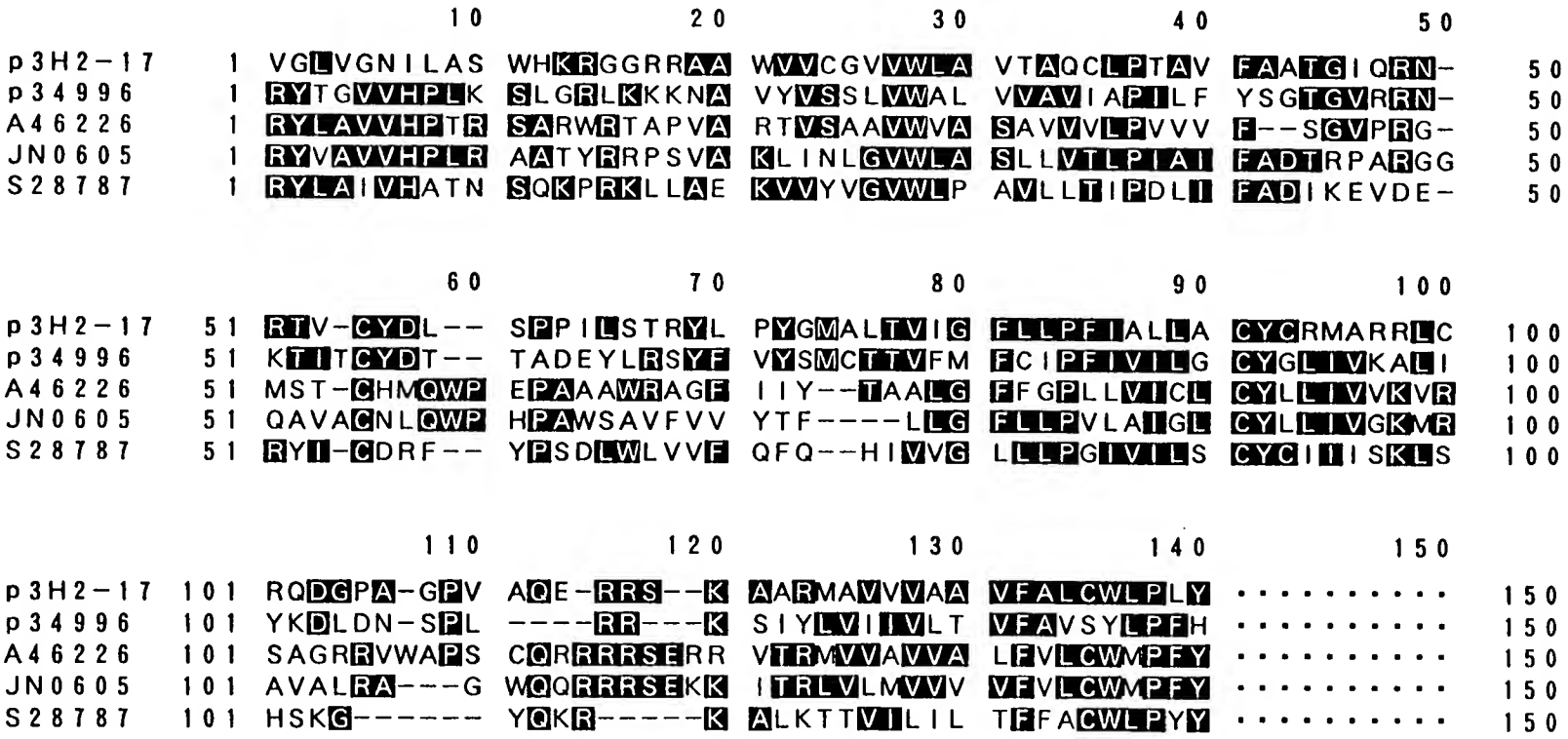

10 20 30 40 50
p3H2-17 1 VGLVGNILAS WHKRGGRRAA WVVCGVVWLA VTAQCLPTAV FAATGIQRN- 50
p34996 1 RYTGVVHPLK SLGRLKKKNA VYVSSLVWAL VVAVIAPILF YSGTGVRRN- 50
A46226 1 RYLAVVHPTR SARWRTAPVA RTVSAAVWVA SAVVVLPVVV F--SGVPRG- 50
JN0605 1 RYVAVVHPLR AATYRRPSVA KLINLGVWLA SLLVTLPIAI FADTRPARGG 50
S28787 1 RYLAIVHATN SQKPRKLLAE KVVYVGVWLP AVLLTIPDLI FADIKEVDE- 50
60 70 80 90 100
p3H2-17 51 RTV-CYDL-- SPPILSTRYL PYGMALTVIG FLLPFIALLA CYCRMARRLC 100
p34996 51 KTITCYDT-- TADEYLRSYF VYSMCTTVFM FCIPFIVILG CYGLIVKALI 100
A46226 51 MST-CHMQWP EPAAAWRAGF IIY--TAALG FFGPLLVICL CYLLIVVKVR 100
JN0605 51 QAVACNLQWP HPAWSAVFVV YTF----LLG FLLPVLAIIGL CYLLIVGKMR 100
S28787 51 RYI-CDRF-- YPSDLWLVVF QFQ--HIVVG LLLPGIVILS CYCIIISKLS 100
110 120 130 140 150
p3H2-17 101 RQDGPA-GPV AQE-RRS--K AARMAVVVAA VFALCWLPLY ·····150
p34996 101 YKDLDN-SPL ----RR---K SIYLVIIVLT VFAVSYLPFH ·····150
A46226 101 SAGRRVWAPS CQRRRRSERR VTRMVVAVVA LFVLCWMPFY ·····150
JN0605 101 AVALRA---G WQQRRRSEKK ITRLVLMVVV VFVLCWMPFY ·····150
S28787 101 HSKG------ YQKR-----K ALKTTVILIL TFFACWLPYY ·····150

FIGURE 40

```
                10                19                28                37                46                55
5'  GTG GGC CTG GTG GGC AAC TTC CTG GCC GCG ATG TCT GTG GAT CGC TAC GTG GCC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Val Gly Leu Val Gly Asn Phe Leu Ala Ala Met Ser Val Asp Arg Tyr Val Ala

                64                73                82                91               100               109
    ATT GTG CAC TCG CGG CGC TCC TCC TCC CTC AGG GTG TCC CGC AAC GCA CTG CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ile Val His Ser Arg Arg Ser Ser Ser Leu Arg Val Ser Arg Asn Ala Leu Leu

               118               127               136               145               154               163
    GGC GTG GGC TTC ATC TGG GCG CTG TCC ATC GCC ATG GCC TCG CCG GTG GCC TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Gly Val Gly Phe Ile Trp Ala Leu Ser Ile Ala Met Ala Ser Pro Val Ala Tyr

               172               181               190               199               208               217
    CAC CAG CGT CTT TTC CAT CGG GAC AGC AAC CAG ACC TTC TGC TGG GAG CAG TGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    His Gln Arg Leu Phe His Arg Asp Ser Asn Gln Thr Phe Cys Trp Glu Gln Trp

               226               235               244               253               262               271
    CCC AAC AAG CTC CAC AAG AAG GCT TAC GTG GTG TGC ACT TTC GTC TTT GGG TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Pro Asn Lys Leu His Lys Lys Ala Tyr Val Val Cys Thr Phe Val Phe Gly Tyr

               280               289               298               307               316               325
    CTT CTG CCC TTA CTG CTC ATC TGC TTT TGC TAT GCC AAG GTC CTT AAT CAT CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Leu Leu Pro Leu Leu Leu Ile Cys Phe Cys Tyr Ala Lys Val Leu Asn His Leu

               334               343               352               361               370               379
    CAT AAA AAG CTG AAA AAC ATG TCA AAA AAG TCT GAA GCA TCC AAG AAA AAG ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    His Lys Lys Leu Lys Asn Met Ser Lys Lys Ser Glu Ala Ser Lys Lys Lys Thr

               388               397               406               415               424               433
    GCA CAG ACC GTC CTG GTG GTC GTT GTA GTA TTT GCC CTC TGC TGG CTG CCT TTC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ala Gln Thr Val Leu Val Val Val Val Val Phe Ala Leu Cys Trp Leu Pro Phe

    TAC 3'
    ---
    Tyr
```

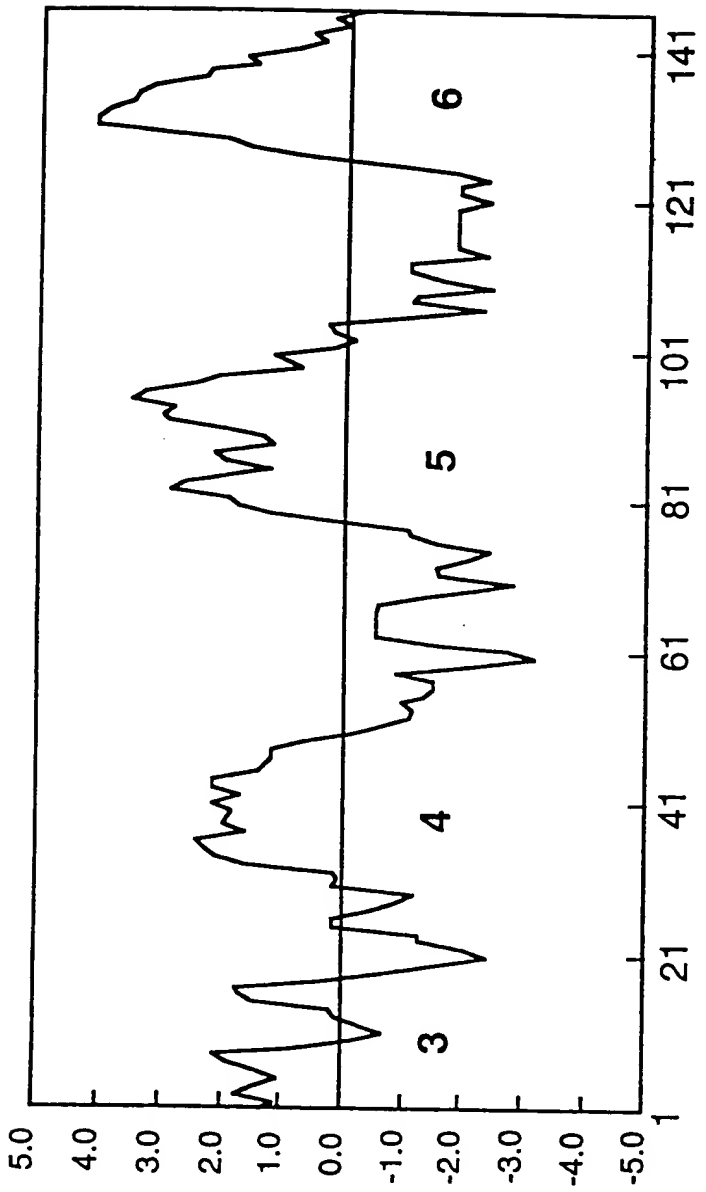


FIGURE 41

FIGURE 42

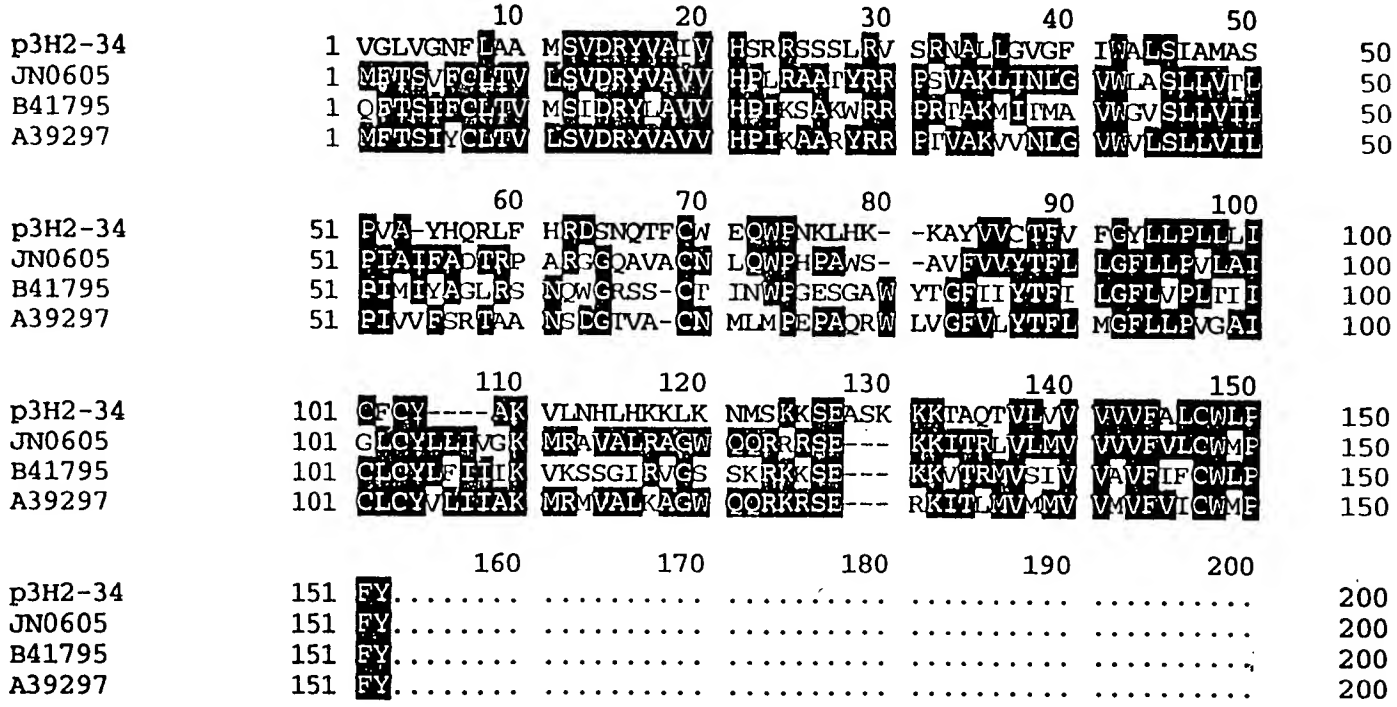


FIGURE 43

```
                10          19          28          37          46          55
5'  GTG GGC ATG GTG GGC AAC GTC CTG GTG CTC TGG TTC TTC GGC TTC TCC ATC AAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Val Gly Met Val Gly Asn Val Leu Val Leu Trp Phe Phe Gly Phe Ser Ile Lys

                64          73          82          91          100         109
    AGG ACC CCC TTC TCC GTC TAC TTC CTG CAC CTG GCC AGC GCC GAC GGC GCC TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Arg Thr Pro Phe Ser Val Tyr Phe Leu His Leu Ala Ser Ala Asp Gly Ala Tyr

                118         127         136         145         154         163
    CTC TTC AGC AAG GCC GTG TTC TCC CTG CTG AAC GCC GGC GGC TTC CTG GGC ACC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Leu Phe Ser Lys Ala Val Phe Ser Leu Leu Asn Ala Gly Gly Phe Leu Gly Thr

                172         181         190         199         208         217
    TTC GCC CAC TAT GTG CGC AGC GTG GCC CGG GTG CTG GGG CTC TGC GCC TTC GTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Phe Ala His Tyr Val Arg Ser Val Ala Arg Val Leu Gly Leu Cys Ala Phe Val

                226         235         244         253         262
    GCG GGC GTG AGC CTC CTG CCG GCC GTG AGC ATG GAG CGC TGC GCG TCT G 3'
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -
    Ala Gly Val Ser Leu Leu Pro Ala Val Ser Met Glu Arg Cys Ala Ser
```

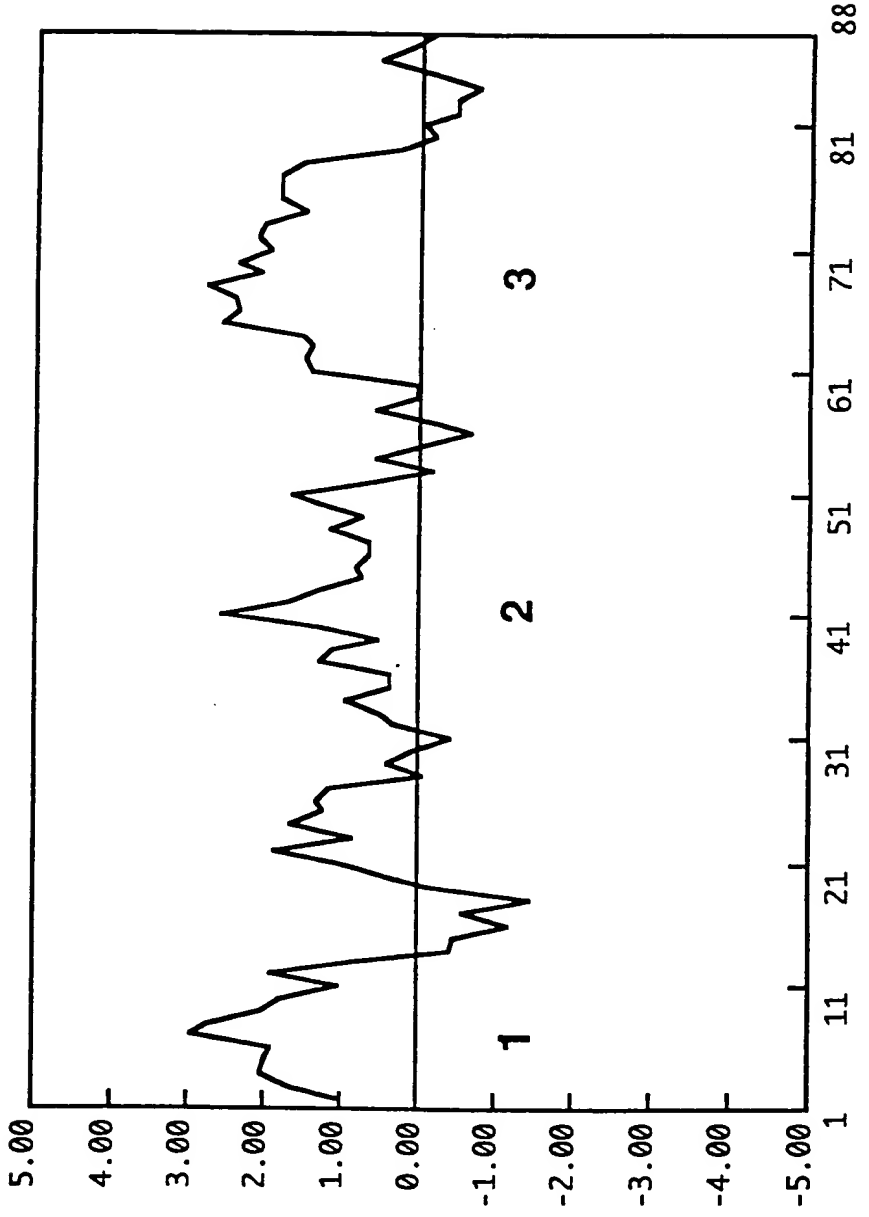
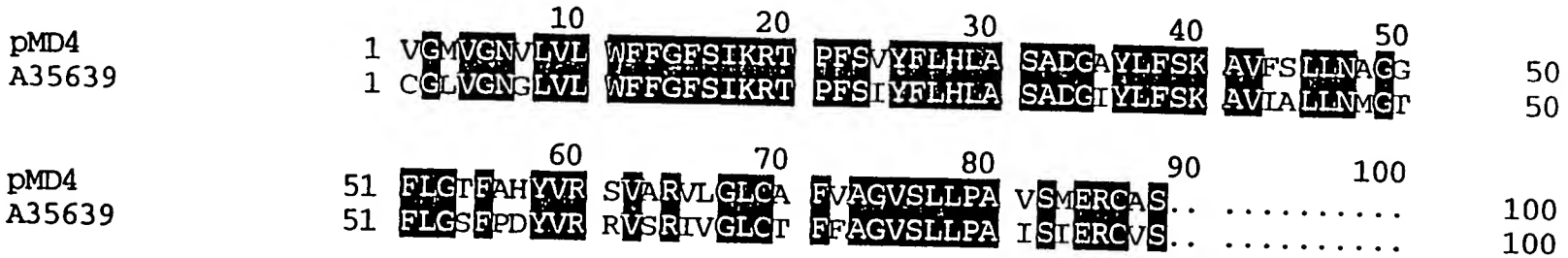


FIGURE 44

FIGURE 45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1 CGLVGNGLVL WFFGFSIKRT PFSIYFLHLA SADGIYLFSK AVIALLNMGT 50
pMD4
A35639
51 FLGTFAHYVR SVARVLGLCA FVAGVSLLPA VSMERCAS.. 100
51 FLGSFPDYVR RVSRIVGLCT FFAGVSLLPA ISIERCVS.. 100

FIGURE 46

```
   1 CAAAGCAACAGGTGCAACCTCAAGGCACTGAAAGCAAGGGGACGCAGCTCACAAGGGCCAAGGGATTGAACC    72
   1                                                                           1

  73 CATAACCGCTCAGAAGATTCTCCGCCTGCGGAGAGCTGCGGAGGAGTCCCACCCGTCCAGCTTGCTGACTGC   144
   1                                                                           1

 145 GAGCAGTGAGAGTCGCCTAGACCCGTACCTCTGTGTTCTGGAGCCTGCCGCCCCCGCACGGGAAAGGCTTAG   216
   1                                                                           1

 217 CTCGGGACTTGCAGCACCGCCTCCTCTTTAGCCAGGCCAGGCACGAGGATAGTGTGATCGGGCACAGCCAGG   288
   1                                                                           1

 289 GTCGCTCTTCCAGGCTTTCTTGCGGGTTGCGGAGGTACTAGTTGGAGACGCGCGCGCTCGCTCTCGCCGCT   360
   1                                                                           1

 361 CTGTCCTGGGCCACTCCGTGATCCTAGGCTACCTCCAGAGCCAGTTTTCCCTGGCTGGCACAACTCTCCAGG   432
   1                                                                           1

 433 GCGCTCCGGTCCGTTGCACAGCGCCCCAAGGGGGTATCCCAGTAAGTGATGGAACTGGCTATGGTGAACCTC   504
   1                                                 MetGluLeuAlaMetValAsnLeu   8

 505 AGTGAAGGGAATGGGAGCGACCCAGAGCCGCCAGCCCCGGAGTCCAGGCCGCTCTTCGGCATTGGCGTGGAG   576
   8 SerGluGlyAsnGlySerAspProGluProProAlaProGluSerArgProLeuPheGlyIleGlyValGlu  32

 577 AACTTCATTACGCTGGTAGTGTTTGGCCTGATTTTCGCGATGGGCGTGCTGGGCAACAGCCTGGTGATCACC   648
  32 AsnPheIleThrLeuValValPheGlyLeuIlePheAlaMetGlyValLeuGlyAsnSerLeuValIleThr  56

 649 GTGCTGGCGCGCAGCAAACCAGGCAAGCCGCGCAGCACCACCAACCTGTTTATCCTCAATCTGAGCATCGCA   720
  56 ValLeuAlaArgSerLysProGlyLysProArgSerThrThrAsnLeuPheIleLeuAsnLeuSerIleAla  80

 721 GACCTGGCCTACCTGCTCTTCTGCATCCCTTTTCAGGCCACCGTGTATGCACTGCCCACCTGGGTGCTGGGC   792
  80 AspLeuAlaTyrLeuLeuPheCysIleProPheGlnAlaThrValTyrAlaLeuProThrTrpValLeuGly 104

 793 GCCTTCATCTGCAAGTTTATACACTACTTCTTCACCGTGTCCATGCTGGTGAGCATCTTCACCCTGGCCGCG   864
 104 AlaPheIleCysLysPheIleHisTyrPhePheThrValSerMetLeuValSerIlePheThrLeuAlaAla 128

 865 ATGTCTGTGGATCGCTACGTGGCCATTGTGCACTCGCGGCGCTCCTCCTCCCTCAGGGTGTCCCGCAACGCA   936
 128 MetSerValAspArgTyrValAlaIleValHisSerArgArgSerSerSerLeuArgValSerArgAsnAla 152

 937 CTGCTGGGCGTGGGCTTCATCTGGGCGCTGTCCATCGCCATGGCCTCGCCGGTGGCCTACCACCAGCGTCTT  1008
 152 LeuLeuGlyValGlyPheIleTrpAlaLeuSerIleAlaMetAlaSerProValAlaTyrHisGlnArgLeu 176

1009 TTCCATCGGGACAGCAACCAGACCTTCTGCTGGGAGCAGTGGCCCAACAAGCTCCACAAGAAGGCTTACGTG  1080
 176 PheHisArgAspSerAsnGlnThrPheCysTrpGluGlnTrpProAsnLysLeuHisLysLysAlaTyrVal 200

1081 GTGTGCACTTTCGTCTTTGGGTACCTTCTGCCCTTACTGCTCATCTGCTTTTGCTATGCCAAGGTCCTTAAT  1152
 200 ValCysThrPheValPheGlyTyrLeuLeuProLeuLeuLeuIleCysPheCysTyrAlaLysValLeuAsn 224

1153 CATCTGCATAAAAAGCTGAAAAACATGTCAAAAAAGTCTGAAGCATCCAAGAAAAAGACTGCACAGACCGTC  1224
 224 HisLeuHisLysLysLeuLysAsnMetSerLysLysSerGluAlaSerLysLysLysThrAlaGlnThrVal 248

1225 CTGGTGGTCGTTGTAGTATTTGGCATATCCTGGCTGCCCCATCATGTCGTCCACCTCTGGGCTGAGTTTGGA  1296
 248 LeuValValValValValPheGlyIleSerTrpLeuProHisHisValValHisLeuTrpAlaGluPheGly 272

1297 GCCTTCCCACTGACGCCAGCTTCCTTCTTCTTCAGAATCACCGCCCATTGCCTGGCATACAGCAACTCCTCA  1368
 272 AlaPheProLeuThrProAlaSerPhePhePheArgIleThrAlaHisCysLeuAlaTyrSerAsnSerSer 296

1369 GTGAACCCCATCATATATGCCTTTCTCTCAGAAAACTTCCGGAAGGCGTACAAGCAAGTGTTCAAGTGTCAT  1440
 296 ValAsnProIleIleTyrAlaPheLeuSerGluAsnPheArgLysAlaTyrLysGlnValPheLysCysHis 320

1441 GTTTGCGATGAATCTCCACGCAGTGAAACTAAGGAAAACAAGAGCCGGATGGACACCCCGCCATCCACCAAC  1512
 320 ValCysAspGluSerProArgSerGluThrLysGluAsnLysSerArgMetAspThrProProSerThrAsn 344

1513 TGCACCCACGTGTGAAGGTTTGCGGGAGCCTCCCGACTTCCAGCTCCCATGTGTGTTAGAGAGAGGAGGGCG  1584
 344 CysThrHisVal***                                                         349

1585 GAGCGAATTATCAAGTAACATGG                                                  1607
 349                                                                         349
```

FIGURE 47

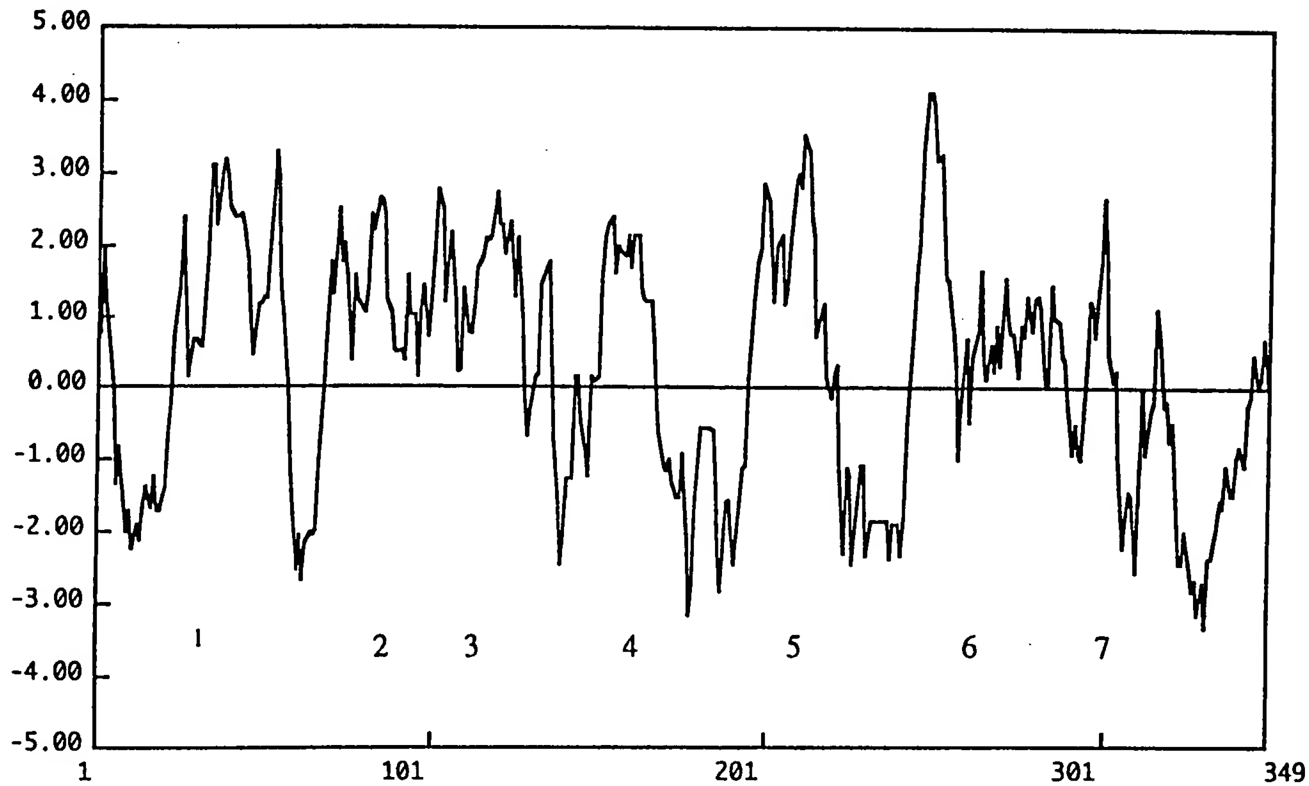
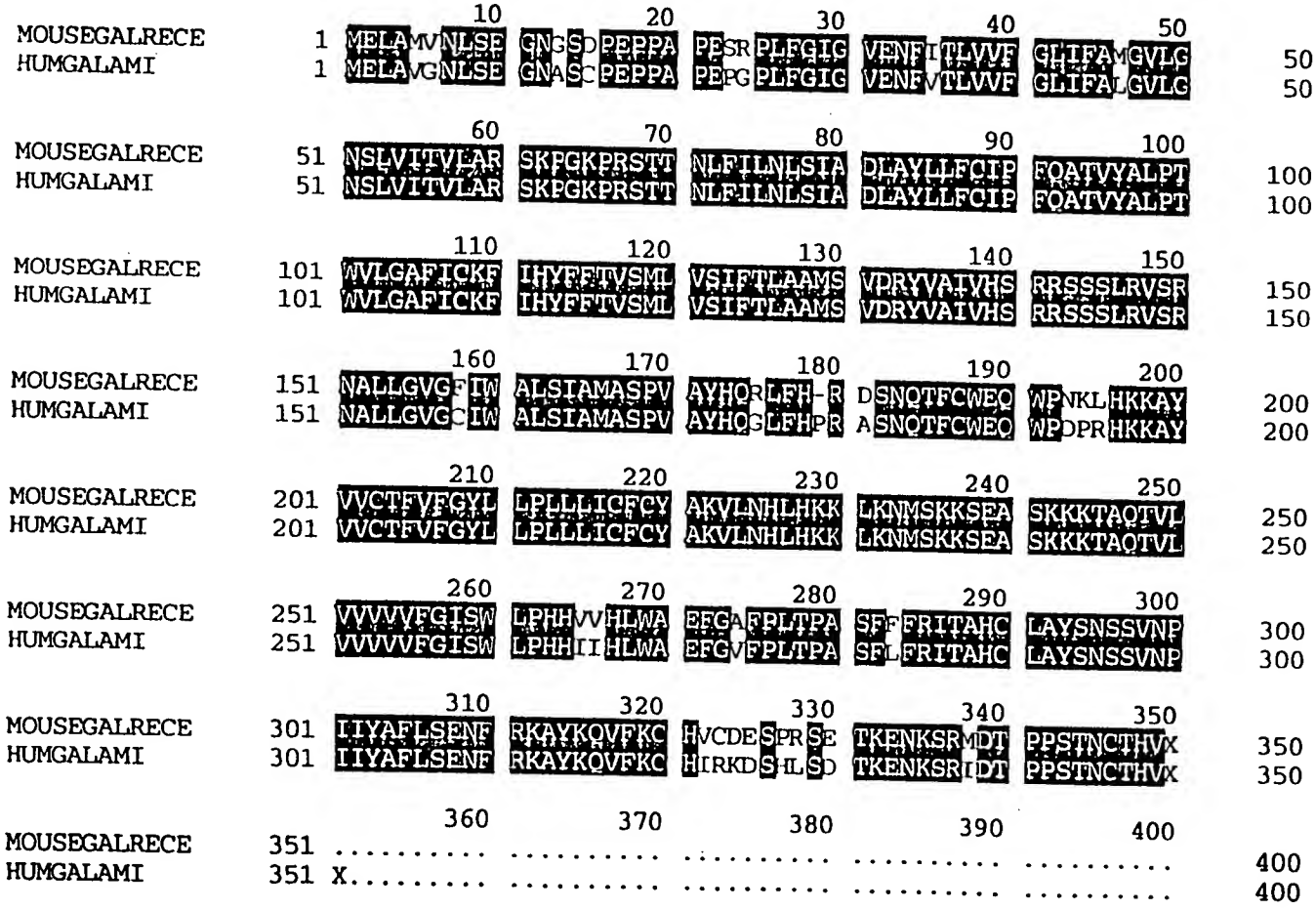


FIGURE 48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HUMGALAMI
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290
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330
340
350
360
370
380
390
400

FIGURE 49

```
                9           18          27                36          45          54
5' CTC GCG GCT CTG GGT ATG GAT CGG TAT CTT CTC ACC CTT CAC CCA GTG TGG TCC
                                       --- --- --- --- --- --- --- --- ---
                                       Leu Leu Thr Leu His Pro Val Trp Ser

           63          72          81          90          99          108
   CAA AAG CAC CGA ACC TCA CAC TGG GCT TCC AGA GTC GTT CTG GGA GTC TGG CTC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Gln Lys His Arg Thr Ser His Trp Ala Ser Arg Val Val Leu Gly Val Trp Leu

           117         126         135         144         153         162
   TCT GCC ACT GCC TTC AGC GTG CCC TAT TTG GTT TTC AGG GAG ACA TAT GAT GAC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Ser Ala Thr Ala Phe Ser Val Pro Tyr Leu Val Phe Arg Glu Thr Tyr Asp Asp

           171         180         189         198         207         216
   CGT AAA GGA AGA GTG ACC TGC AGA AAT AAC TAC GCT GTG TCC ACT GAC TGG GAA
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Arg Lys Gly Arg Val Thr Cys Arg Asn Asn Tyr Ala Val Ser Thr Asp Trp Glu

           225         234         243         252         261         270
   AGC AAA GAG ATG CAA ACA GTA AGA CAA TGG ATT CAT GCC ACC TGT TTC ATC AGC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Ser Lys Glu Met Gln Thr Val Arg Gln Trp Ile His Ala Thr Cys Phe Ile Ser

           279         288         297         306         315         324
   CGC TTC ATA CTG GGC TTC CTT CTG CCT TTC TTA GTC ATT GGC TTT TGT TAT GAA
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Arg Phe Ile Leu Gly Phe Leu Leu Pro Phe Leu Val Ile Gly Phe Cys Tyr Glu

           333         342         351         360         369         378
   AGA GTA GCC CGC AAG ATG AAA GAG AGG GGC CTC TTT AAA TCC AGC AAA CCC TTC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Arg Val Ala Arg Lys Met Lys Glu Arg Gly Leu Phe Lys Ser Ser Lys Pro Phe

           387         396         405         414         423         432
   AAA GTC ACG ATG ACT GCT GTT ATC TCT TTT TTC TGT CCT GGC TTC CCT ACC ACA
   --- --- --- --- --- --- --- --- ---
   Lys Val Thr Met Thr Ala Val Ile

   TG 3'
```

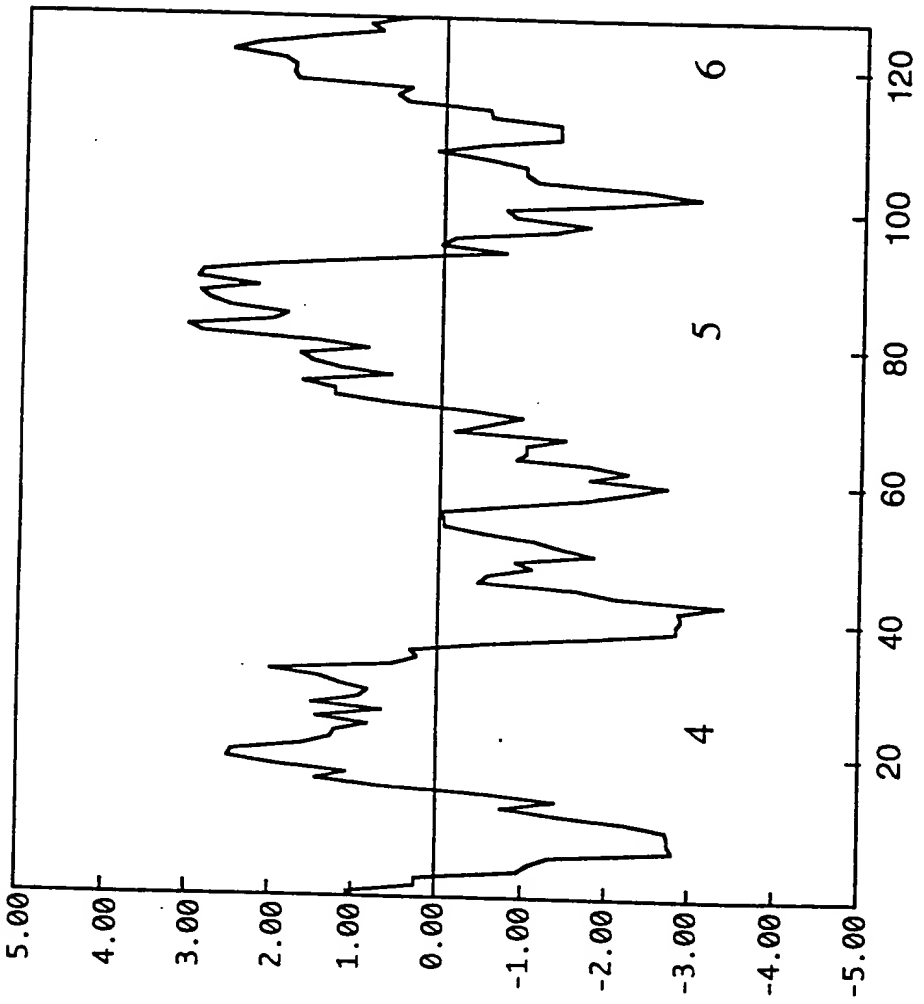


FIGURE 50

FIGURE 51

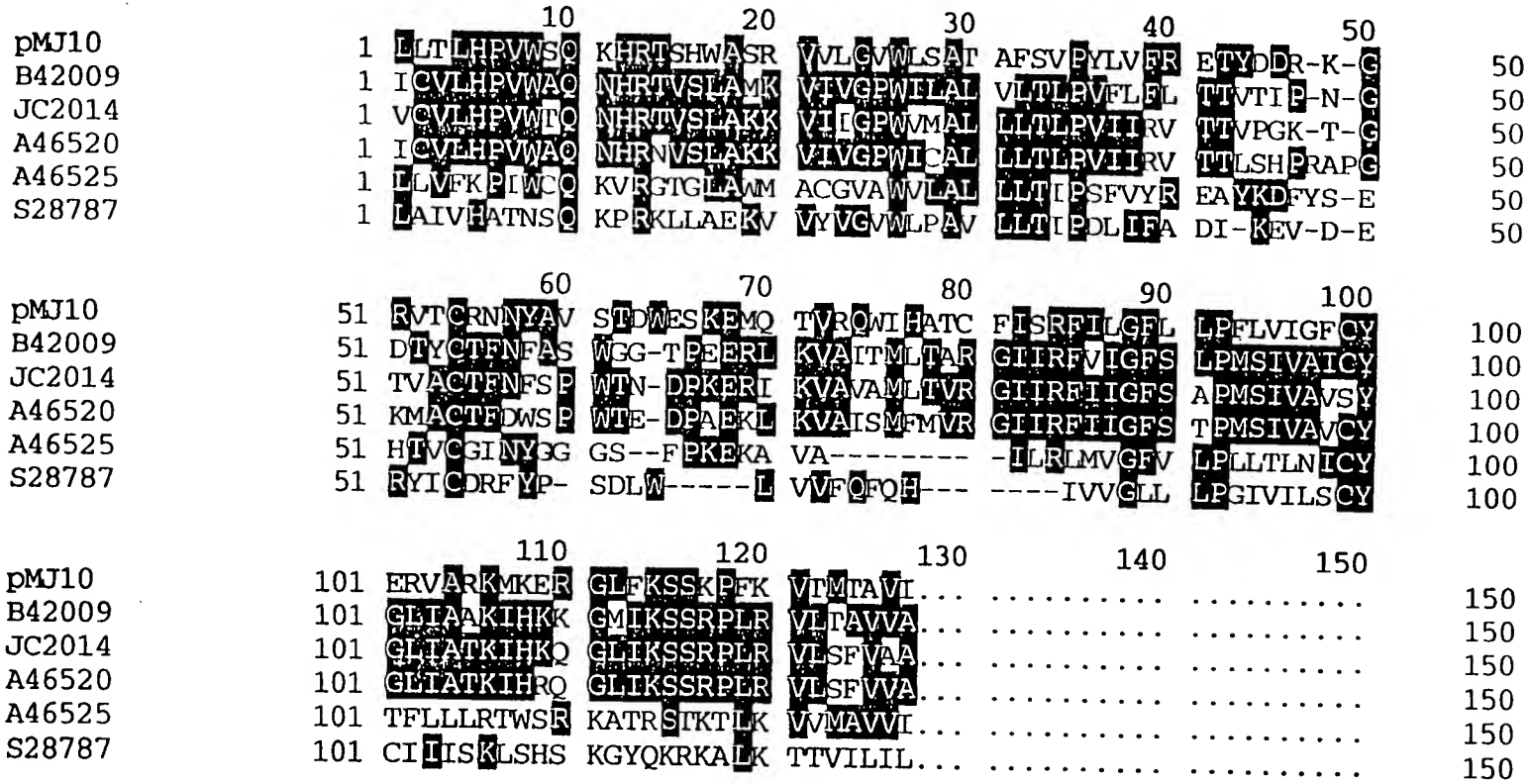
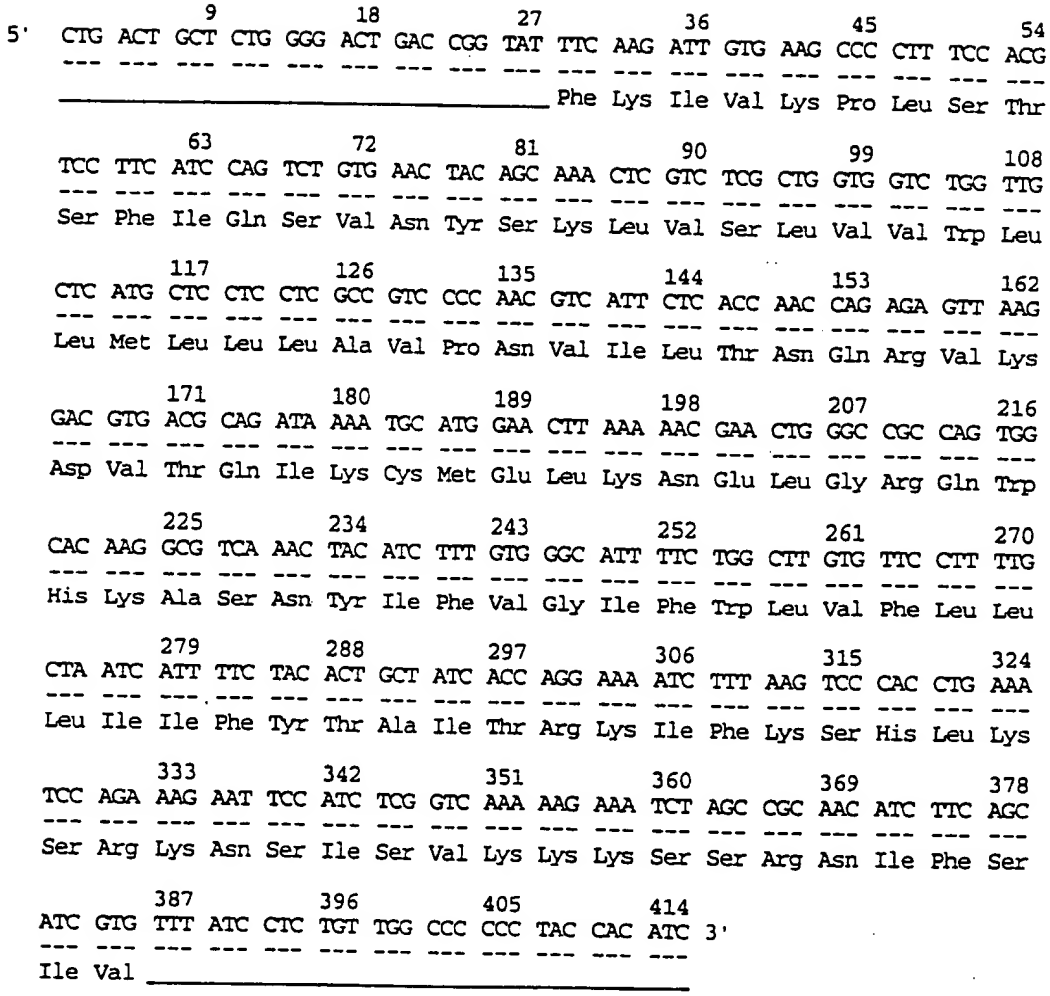


FIGURE 52


5' CTG ACT GCT CTG GGG ACT GAC CGG TAT TTC AAG ATT GTG AAG CCC CTT TCC ACG
Phe Lys Ile Val Lys Pro Leu Ser Thr
TCC TTC ATC CAG TCT GTG AAC TAC AGC AAA CTC GTC TCG CTG GTG GTC TGG TTG
Ser Phe Ile Gln Ser Val Asn Tyr Ser Lys Leu Val Ser Leu Val Val Trp Leu
CTC ATG CTC CTC CTC GCC GTC CCC AAC GTC ATT CTC ACC AAC CAG AGA GTT AAG
Leu Met Leu Leu Leu Ala Val Pro Asn Val Ile Leu Thr Asn Gln Arg Val Lys
GAC GTG ACG CAG ATA AAA TGC ATG GAA CTT AAA AAC GAA CTG GGC CGC CAG TGG
Asp Val Thr Gln Ile Lys Cys Met Glu Leu Lys Asn Glu Leu Gly Arg Gln Trp
CAC AAG GCG TCA AAC TAC ATC TTT GTG GGC ATT TTC TGG CTT GTG TTC CTT TTG
His Lys Ala Ser Asn Tyr Ile Phe Val Gly Ile Phe Trp Leu Val Phe Leu Leu
CTA ATC ATT TTC TAC ACT GCT ATC ACC AGG AAA ATC TTT AAG TCC CAC CTG AAA
Leu Ile Ile Phe Tyr Thr Ala Ile Thr Arg Lys Ile Phe Lys Ser His Leu Lys
TCC AGA AAG AAT TCC ATC TCG GTC AAA AAG AAA TCT AGC CGC AAC ATC TTC AGC
Ser Arg Lys Asn Ser Ile Ser Val Lys Lys Lys Ser Ser Arg Asn Ile Phe Ser
ATC GTG TTT ATC CTC TGT TGG CCC CCC TAC CAC ATC 3'
Ile Val

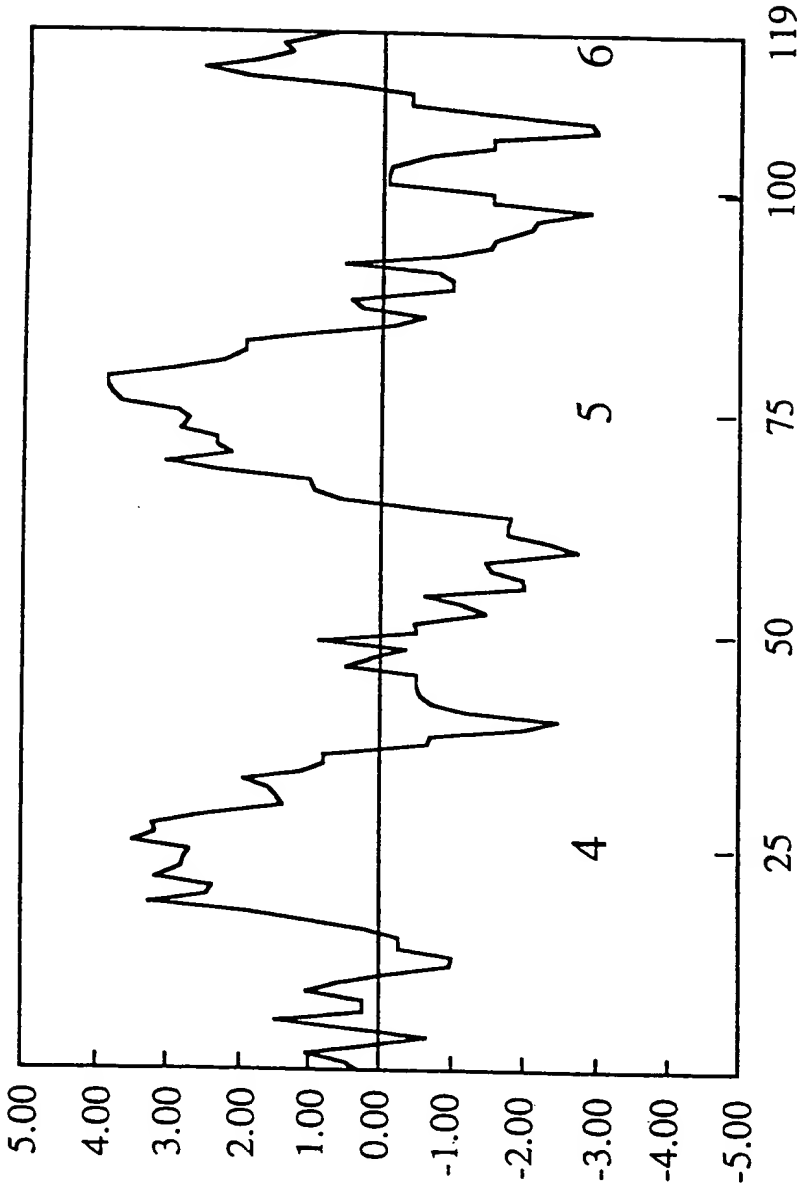
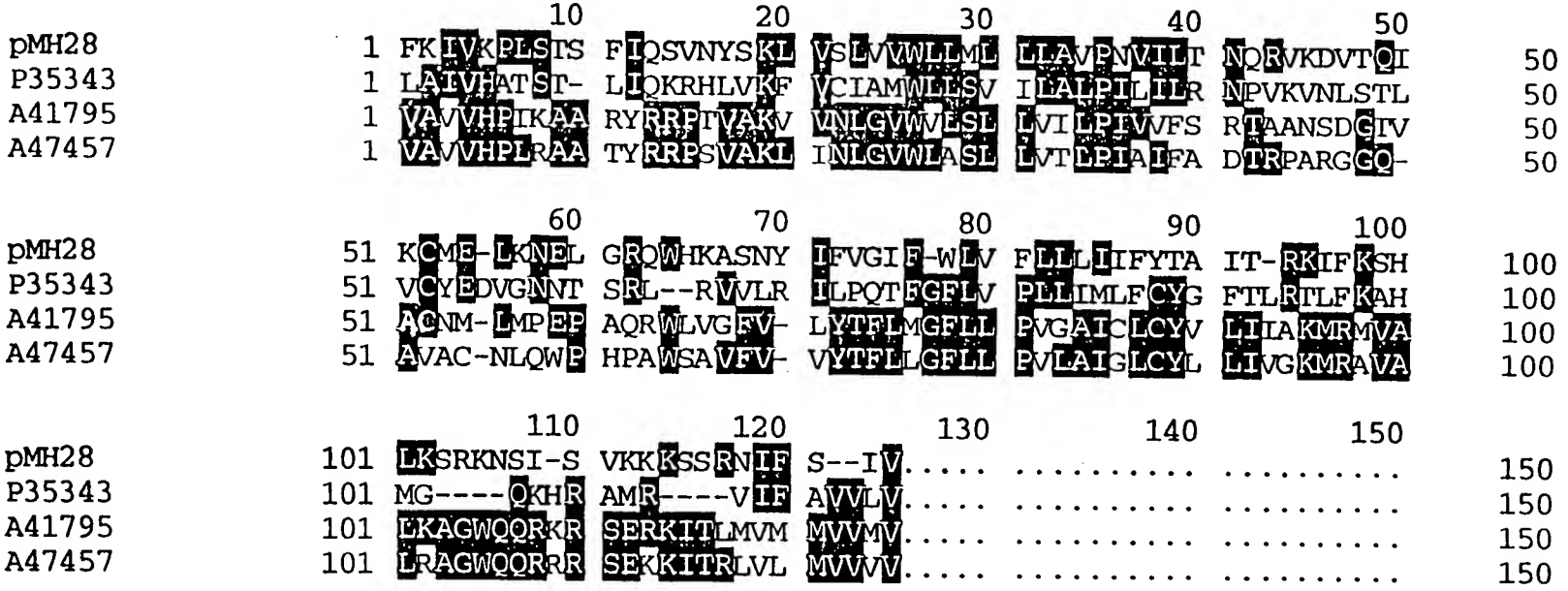


FIGURE 53

FIGURE 54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P35343 1 LAIVHATST- LIQKRHLVKF VCIAMWLLSV ILALPILILR NPVKVNLSTL 50
A41795 1 VAVVHPIKAA RYRRPTVAKV VNLGVWVLSL LVILPIVVFS RTAANSDGIV 50
A47457 1 VAVVHPLRAA TYRRPSVAKL INLGVWLASL LVTLPIAIFA DTRPARGGQ- 50
60 70 80 90 100
pMH28 51 KCME-LKNEL GRQWHKASNY IFVGIF-WLV FLLLIIFYTA IT-RKIFKSH 100
P35343 51 VCYEDVGNNT SRL--RVVLR ILPQTFGFLV PLLIMLFCYG FTLRTLFKAH 100
A41795 51 ACNM-LMPEP AQRWLVGFV- LYTFLMGFLL PVGAICLCYV LIIAKMRMVA 100
A47457 51 AVAC-NLQWP HPAWSAVFV- VYTFLLGFLL PVLAIGLCYL LIVGKMRAVA 100
110 120 130 140 150
pMH28 101 LKSRKNSI-S VKKKSSRNIF S--IV..... 150
P35343 101 MG----QKHR AMR----VIF AVVLV..... 150
A41795 101 LKAGWQQRKR SERKITLMVM MVVMV..... 150
A47457 101 LRAGWQQRRR SEKKITRLVL MVVVV..... 150

FIGURE 55

```
                            9          18          27          36          45          54
5'  GCC ACC AAC GTG TTC ATC CTG TGT CTG GTG GAC CTG CTG GCT GCC CTG ACC CTC
                                       --- --- --- --- --- --- --- --- ---
                                       Val Asp Leu Leu Ala Ala Leu Thr Leu

            63          72          81          90          99         108
    ATG CCT CTG GCC ATG CTC TCC AGC TCC GCC CTC TTT GAC CAC GCC CTC TTT GGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Met Pro Leu Ala Met Leu Ser Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly

           117         126         135         144         153         162
    GAG GTG GCC TGC CGC CTC TAC TTG TTC CTG AGC GTC TGC TTT GTC AGC CTG GCC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Glu Val Ala Cys Arg Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu Ala

           171         180         189         198         207         216
    ATC CTC TCG GTG TCC GCC ATC AAT GTG GAG CGC TAC TAT TAT GTG GTC CAC CCC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ile Leu Ser Val Ser Ala Ile Asn Val Glu Arg Tyr Tyr Tyr Val Val His Pro

           225         234         243         252         261         270
    ATG CGC TAT GAG GTG CGC ATG AAA CTG GGG CTG GTG GCC TCT GTG CTG GTG GGC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Met Arg Tyr Glu Val Arg Met Lys Leu Gly Leu Val Ala Ser Val Leu Val Gly

           279         288         297         306         315         324
    GTG TGG GTG AAG GCC CTG GCC ATG GCT TCT GTG CCA GTG TTG GGA AGG GTG TCC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Val Trp Val Lys Ala Leu Ala Met Ala Ser Val Pro Val Leu Gly Arg Val Ser

           333         342         351         360         369         378
    TGG GAG GAA GGC CCT CCC AGT GTC CCC CCA GGC TGT TCA CTC CAA TGG AGC CAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Trp Glu Glu Gly Pro Pro Ser Val Pro Pro Gly Cys Ser Leu Gln Trp Ser His

           387         396         405         414         423         432
    AGT GCC TAC TGC CAG CTT TTC GTG GTG GTC TTC GCC GTC CTC TAC TTC CTG CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ser Ala Tyr Cys Gln Leu Phe Val Val Val Phe Ala Val Leu Tyr Phe Leu Leu

           441         450         459         468         477         486
    CCC CTG CTC CTC ATC CTT GTG GTC TAC TGC AGC ATG TTC CGG GTG GCT CGT GTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Pro Leu Leu Leu Ile Leu Val Val Tyr Cys Ser Met Phe Arg Val Ala Arg Val

           495         504         513         522         531         540
    GCT GCC ATG CAG CAC GGG CCG CTG CCC ACG TGG ATG GAG ACG CCC CGG CAA CGC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ala Ala Met Gln His Gly Pro Leu Pro Thr Trp Met Glu Thr Pro Arg Gln Arg
```

FIGURE 56

549 558 567 576 585 594

TCC GAG TCT CTC AGC AGC CGC TCC ACT ATG GTC ACC AGC TCG GGG GCC CCG CAG

Ser Glu Ser Leu Ser Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala Pro Gln

603 612 621 630 639 648

ACC ACC CCT CAC CGG ACG TTT GGC GGA GGG AAG GCA GCA GTG GTC CTC CTG GCT

Thr Thr Pro His Arg Thr Phe Gly Gly Gly Lys Ala Ala Val Val Leu Leu Ala

657 666 675 684 693 702

GTG GGA GGA CAG TTC CTG CTC TGT TGG TTG CCC TAC TTC TCC TTC CAC CTC TAT

Val Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe Ser Phe His Leu Tyr

711 720 729 738 747 756

GTG GCC CTG AGC GCT CAG CCC ATT GCA GCG GGG CAG GTG GAG AAC GTG GTG ACC

Val Ala Leu Ser Ala Gln Pro Ile Ala Ala Gly Gln Val Glu Asn Val Val Thr

765 774 783 792 801 810

TGG ATT GGC TAC TTC TGC TTC ACC TCC <u>AAC CCT CTC CTC TAT TCC TTC CTC CCT</u> 3'

Trp Ile Gly Tyr Phe Cys Phe Thr Ser

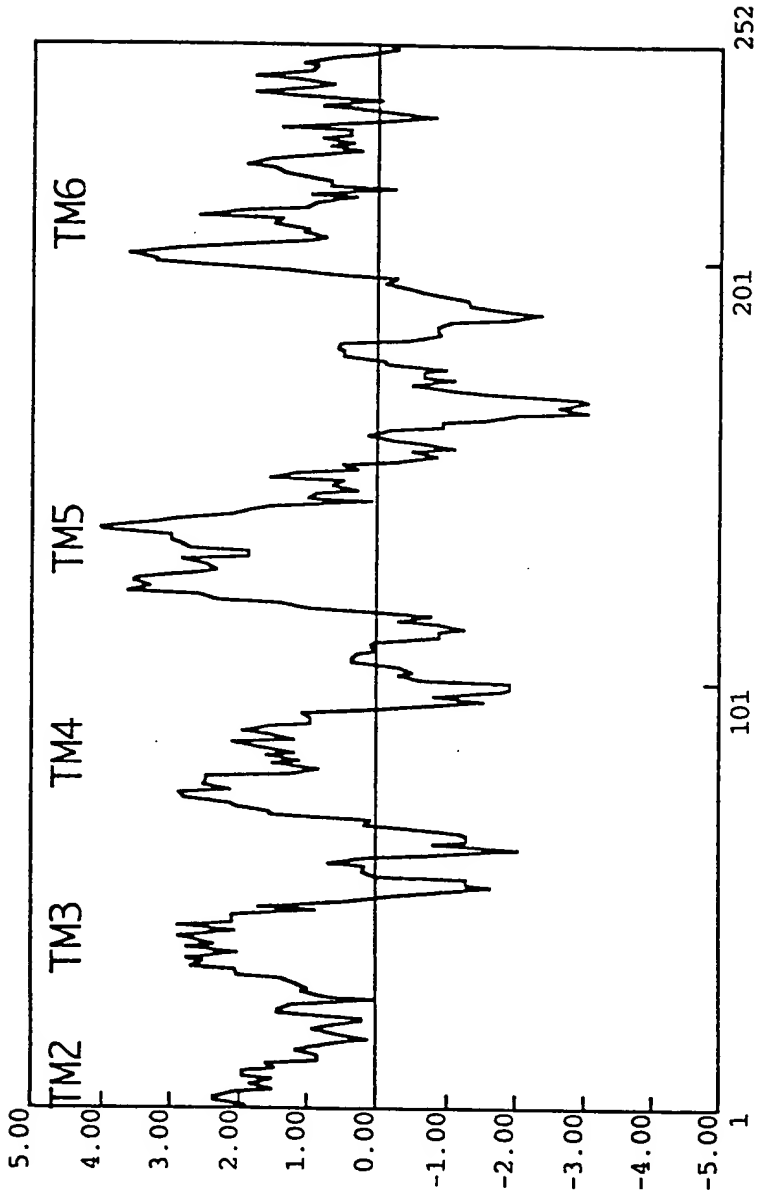


FIGURE 57

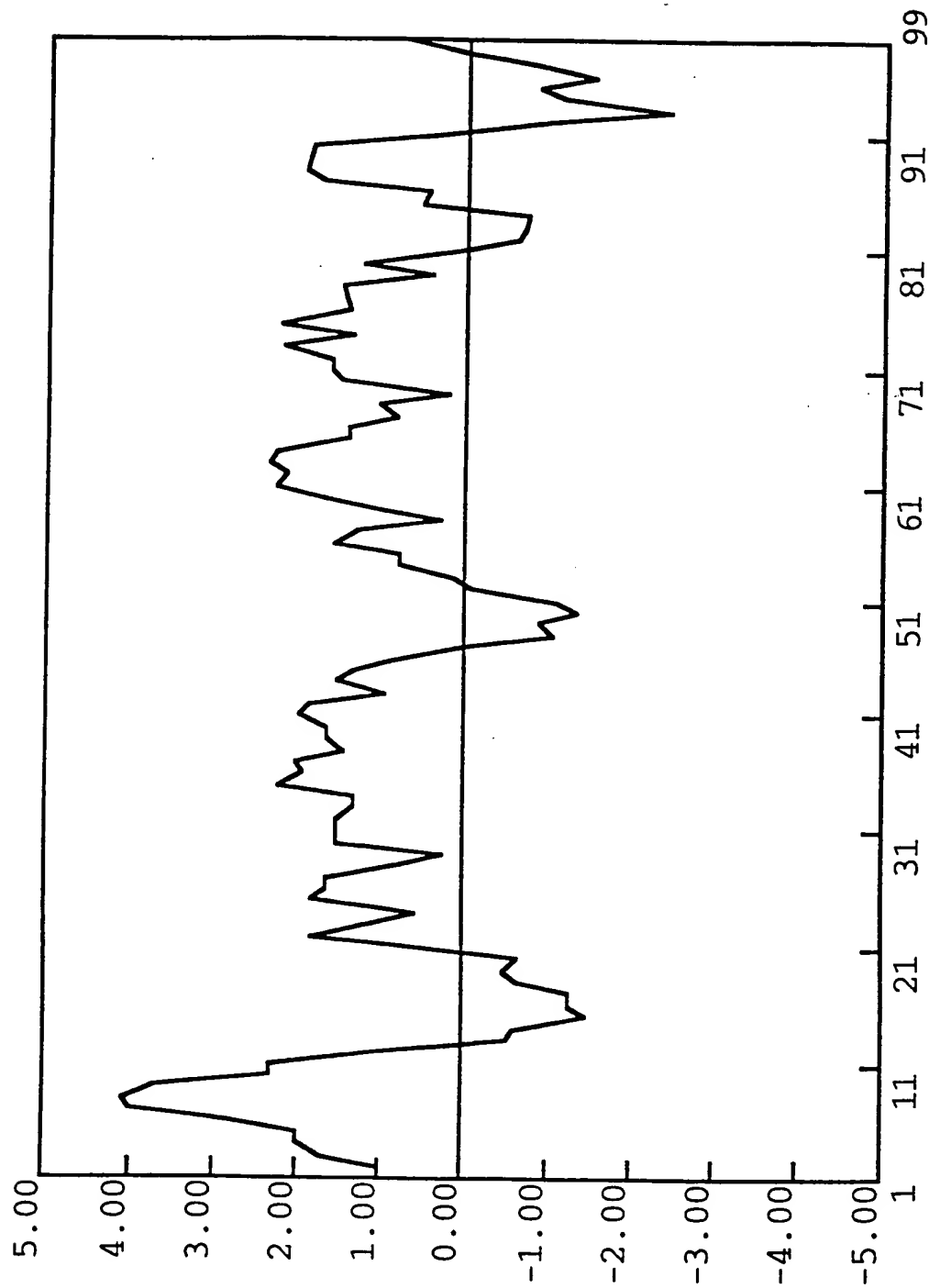


FIGURE 58

FIGURE 59

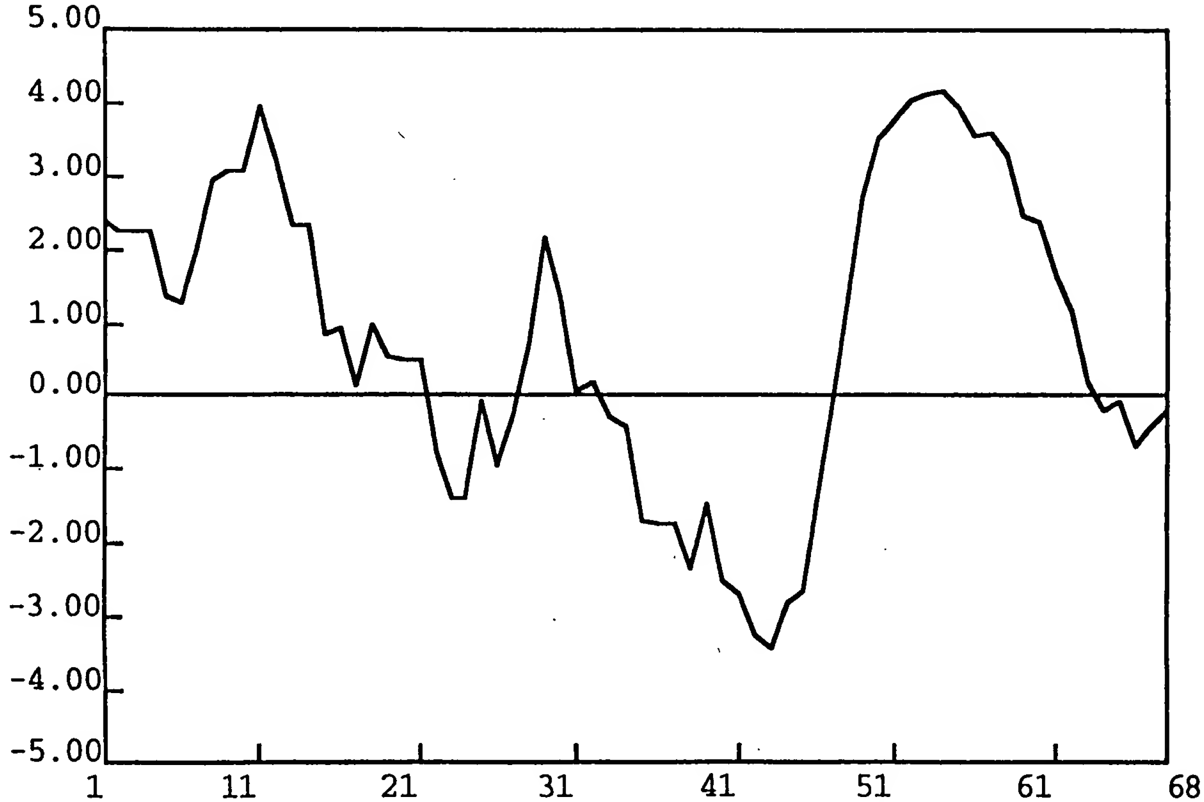
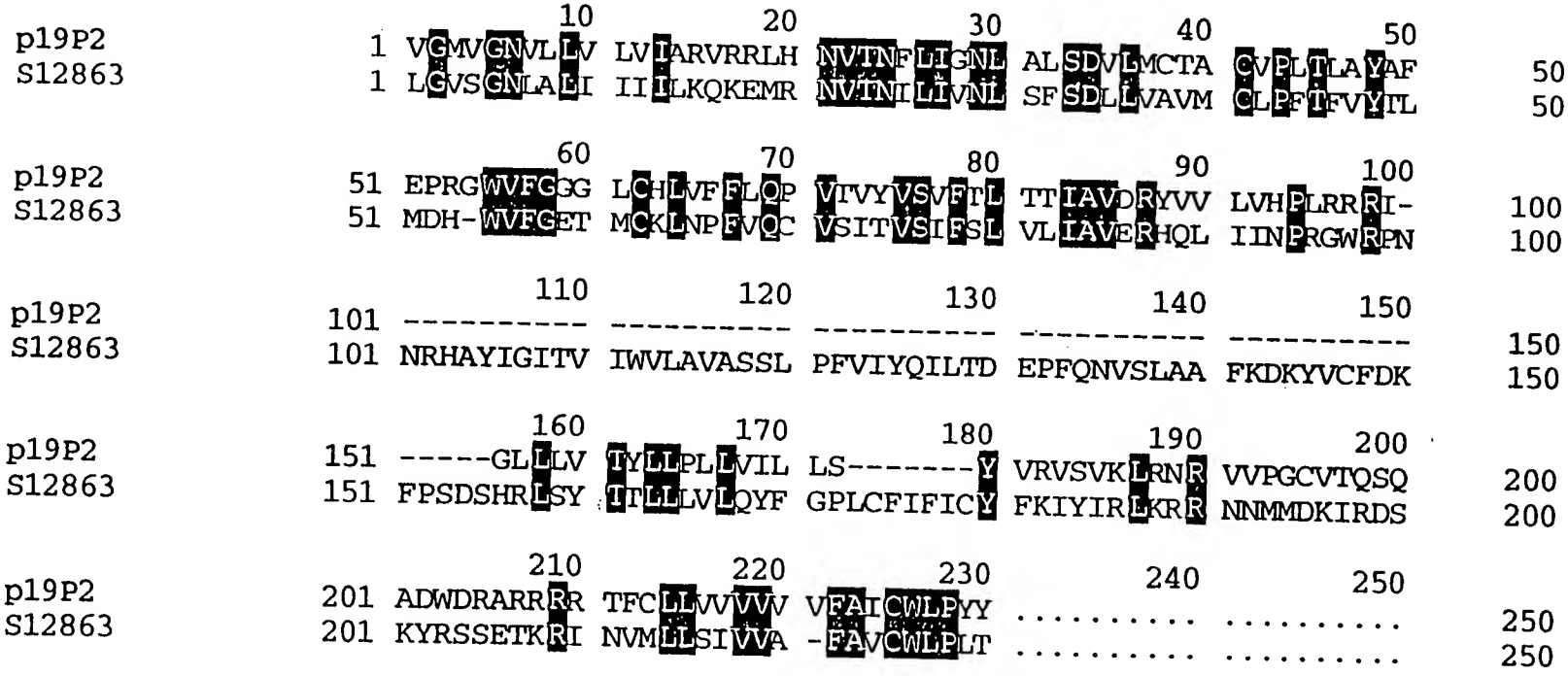


FIGURE 60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S12863
10 20 30 40 50
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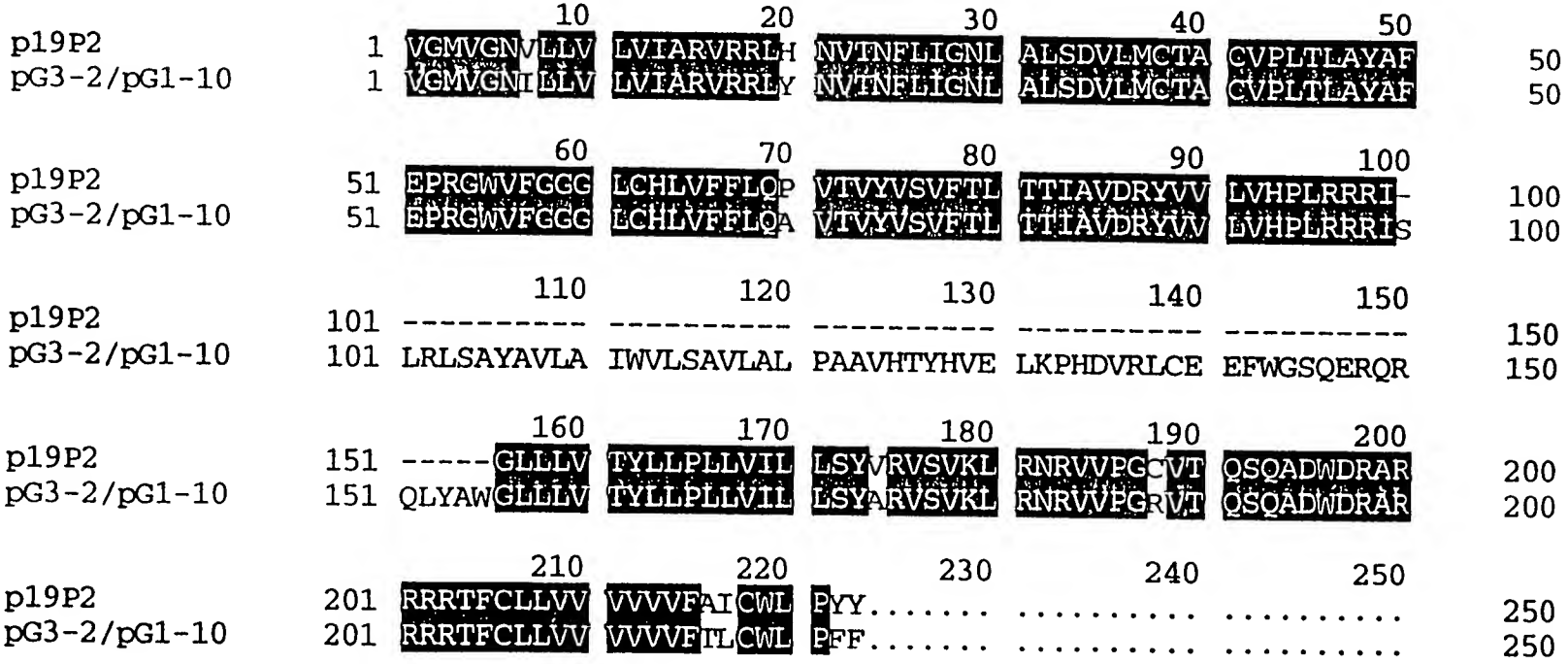
1 LGVSGNLALI IILLKQKEMR NVTNILIVNL SFSDLLVAVM CLPFTFVYTL 50
60 70 80 90 100
51 EPRGWVFGGG LCHLVFFLQP VTVYVSVFTL TTIAVDRYVV LVHPLRRRI- 100
51 MDH-WVFGET MCKLNPFVQC VSITVSIFSL VLIAVERHQL IINPRGWRPN 100
110 120 130 140 150
101 ---------- ---------- ---------- ---------- ---------- 150
101 NRHAYIGITV IWVLAVASSL PFVIYQILTD EPFQNVSLAA FKDKYVCFDK 150
160 170 180 190 200
151 -----GLLLV TYLLPLLVIL LS-------Y VRVSVKLRNR VVPGCVTQSQ 200
151 FPSDSHRLSY TTLLLVLQYF GPLCFIFICY FKIYIRLKRR NNMMDKIRDS 200
210 220 230 240 250
201 ADWDRARRRR TFCLLVVVVV VFAICWLPYY 250
201 KYRSSETKRI NVMLLSIVVA -FAVCWLPLT 250

FIGURE 61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p19P2 1 VGMVGNVLLV LVIARVRRLH NVTNFLIGNL ALSDVLMCTA CVPLTLAYAF 50
pG3-2/pG1-10 1 VGMVGNILLV LVIARVRRLY NVTNFLIGNL ALSDVLMGTA CVPLTLAYAF 50
60 70 80 90 100
p19P2 51 EPRGWVFGGG LCHLVFFLQP VTVYVSVFTL TTIAVDRYVV LVHPLRRRI- 100
pG3-2/pG1-10 51 EPRGWVFGGG LCHLVFFLQA VTVYVSVFTL TTIAVDRYVV LVHPLRRRIS 100
110 120 130 140 150
p19P2 101 ---------- ---------- ---------- ---------- ---------- 150
pG3-2/pG1-10 101 LRLSAYAVLA IWVLSAVLAL PAAVHTYHVE LKPHDVRLCE EFWGSQERQR 150
160 170 180 190 200
p19P2 151 -----GLLLV TYLLPLLVIL LSYVRVSVKL RNRVVPGCVT QSQADWDRAR 200
pG3-2/pG1-10 151 QLYAWGLLLV TYLLPLLVIL LSYARVSVKL RNRVVPGRVT QSQADWDRAR 200
210 220 230 240 250
p19P2 201 RRRTFCLLVV VVVVFAICWL PYY..... 250
pG3-2/pG1-10 201 RRRTFCLLVV VVVVFTLCWL PFF..... 250

FIGURE 62

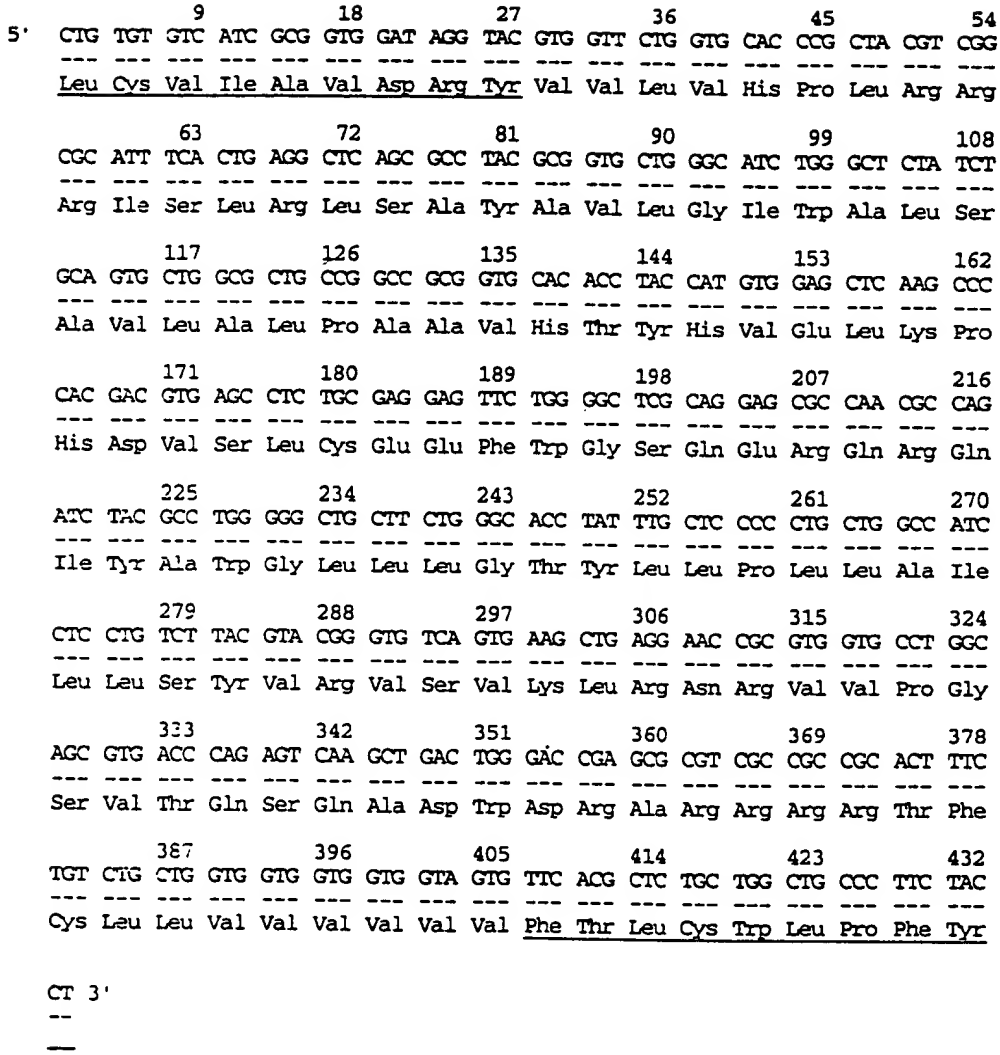
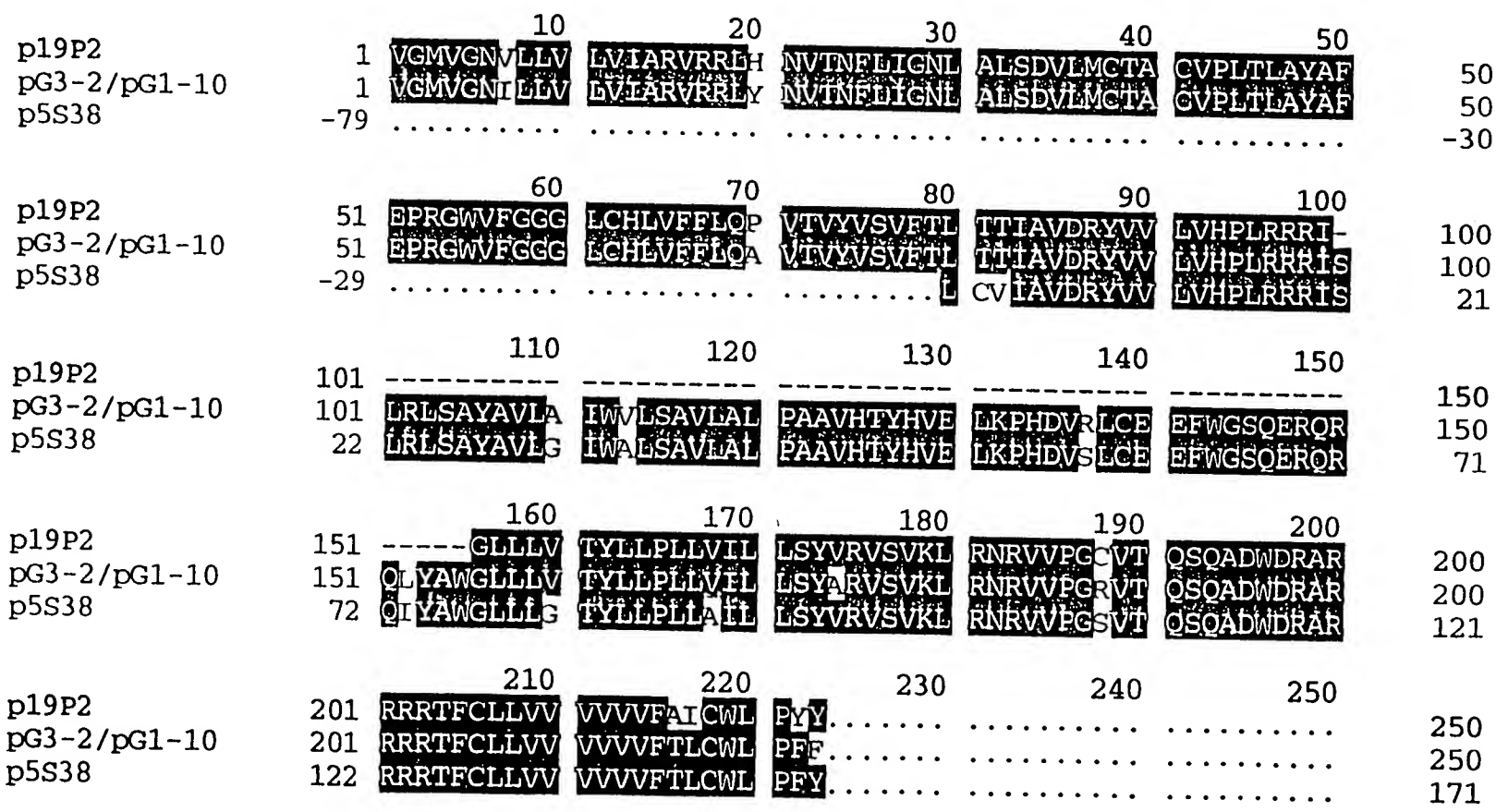


FIGURE 63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p5S38
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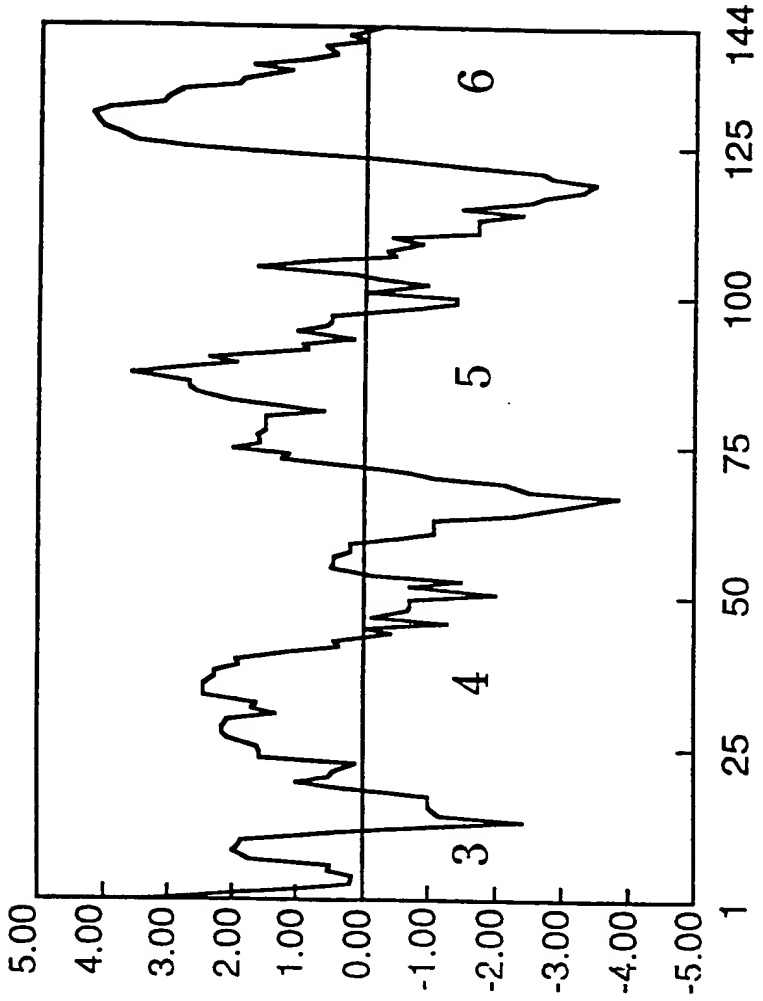


FIGURE 64

FIGURE 65

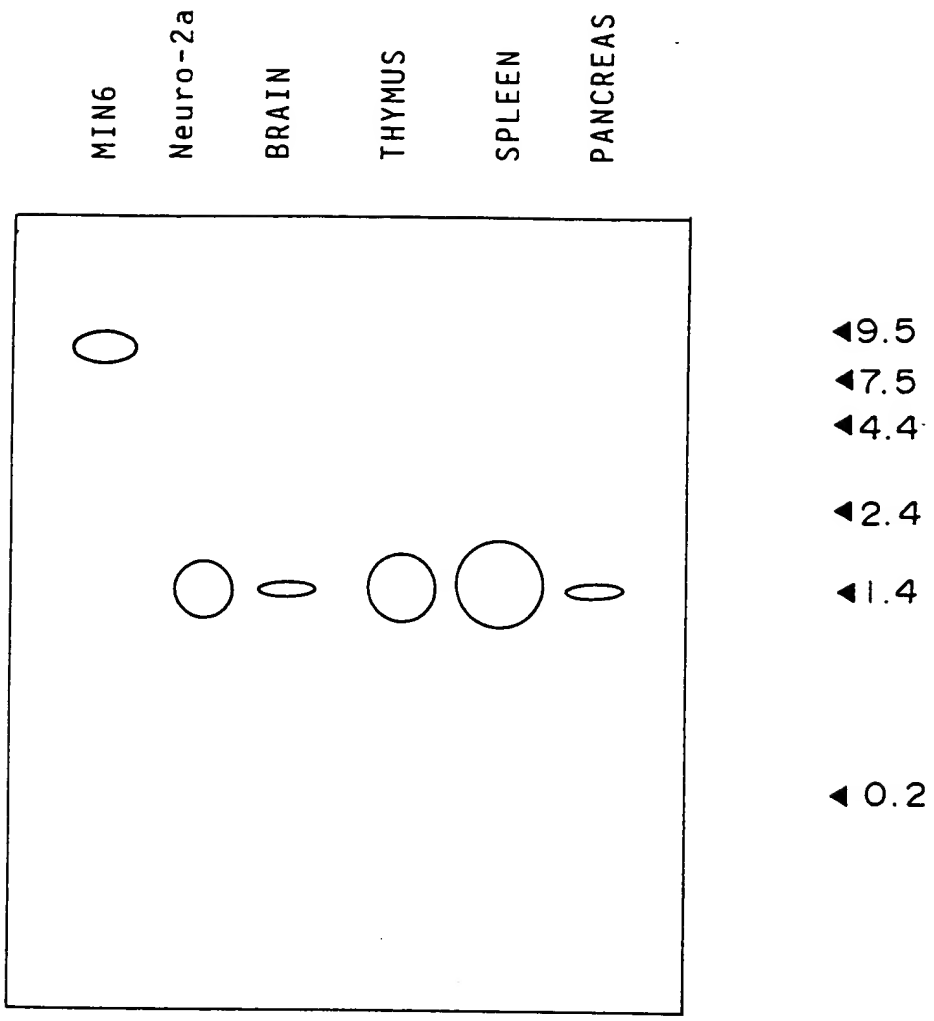


FIGURE 66

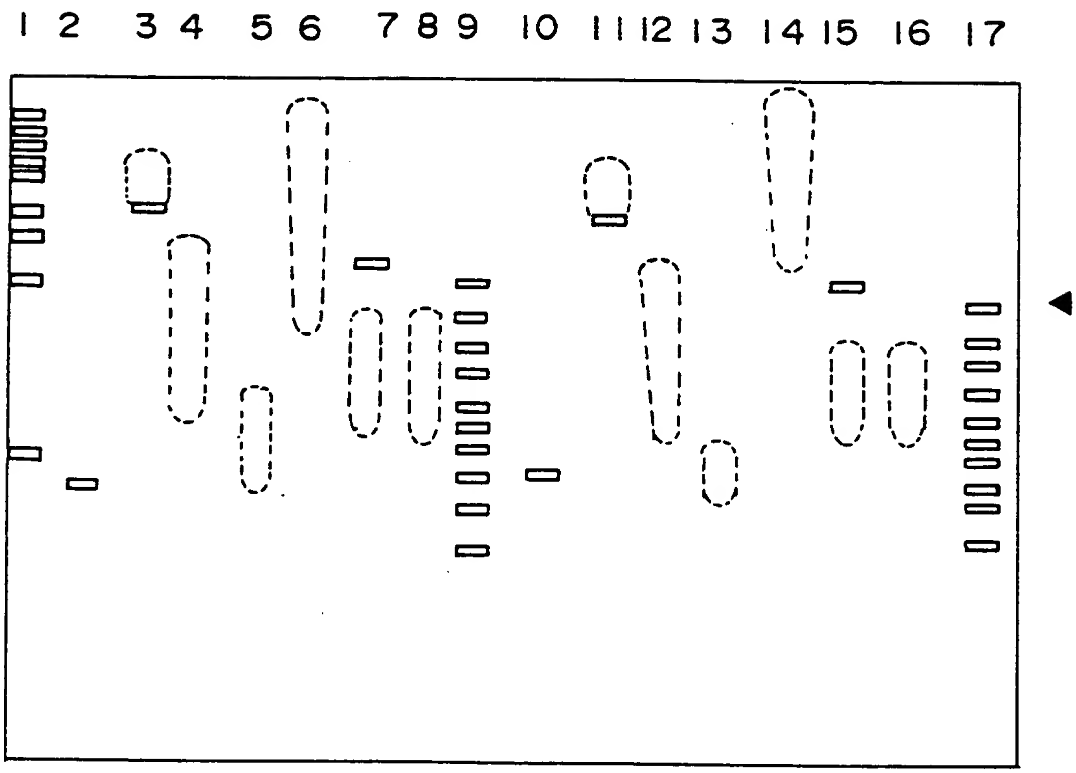


FIGURE 67

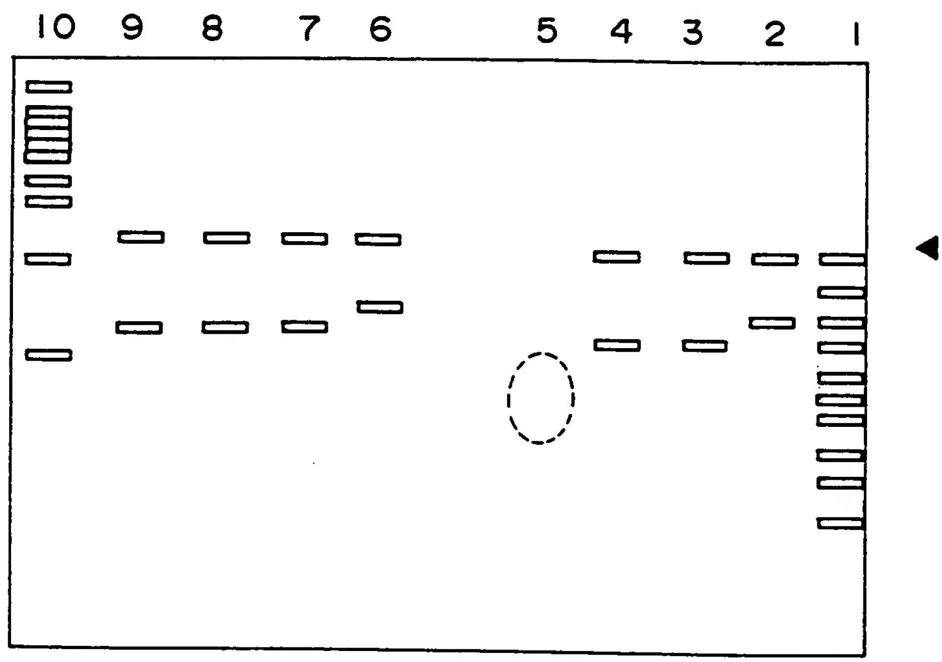
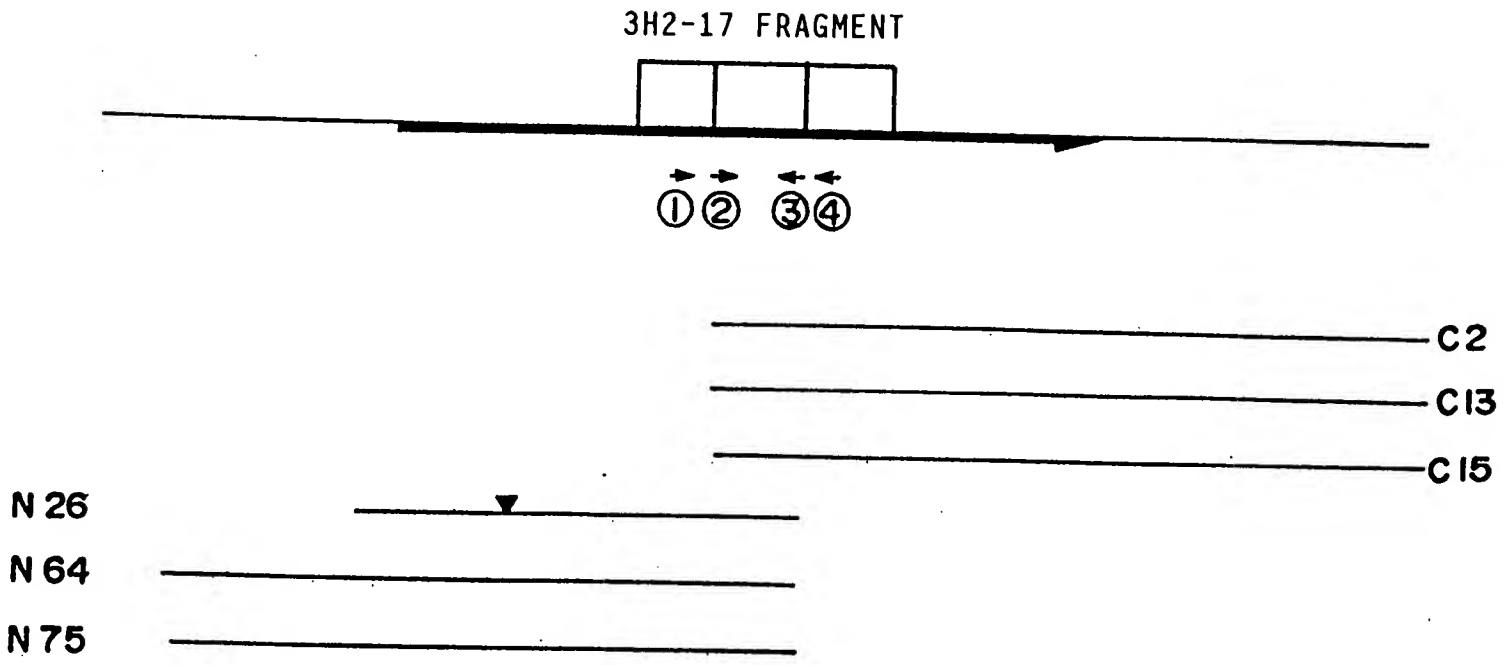


FIGURE 68



C2 SPLEEN DERIVED C13 C15 THYMUS DERIVED
N75 SPLEEN DERIVED N26 N64 THYMUS DERIVED
▼ PCR ERROR SITE

FIGURE 69

```
   1 GAGCATAGGAAAGGCTGACAGGCAGTTATGGAGCAGGACAATGGCACCATCCAGGCTCCA     60
   1                                MetGluGlnAspAsnGlyThrIleGlnAlaPro     11

  61 GGCTTGCCGCCCACCACCTGCGTCTACCGTGAGGATTTCAAGCGACTGCTGCTAACCCCG    120
  11 GlyLeuProProThrThrCysValTyrArgGluAspPheLysArgLeuLeuLeuThrPro     31

 121 GTATACTCGGTGGTGCTGGTGGTCGGCCTGCCACTGAACATCTGCGTCATTGCCCAGATC    180
  31 ValTyrSerValValLeuValValGlyLeuProLeuAsnIleCysValIleAlaGlnIle     51

 181 TGCGCATCCCGCCGGACCCTGACCCGTTCCGCTGTGTACACCCTGAACCTGGCACTGGCG    240
  51 CysAlaSerArgArgThrLeuThrArgSerAlaValTyrThrLeuAsnLeuAlaLeuAla     71

 241 GACCTGATGTATGCCTGTTCACTACCCCTACTTATCTATAACTACGCCAGAGGGGACCAC    300
  71 AspLeuMetTyrAlaCysSerLeuProLeuLeuIleTyrAsnTyrAlaArgGlyAspHis     91

 301 TGGCCCTTCGGAGACCTCGCCTGCCGCTTTGTACGCTTCCTCTTCTATGCCAATCTACAT    360
  91 TrpProPheGlyAspLeuAlaCysArgPheValArgPheLeuPheTyrAlaAsnLeuHis    111

 361 GGCAGCATCCTGTTCCTCACCTGCATTAGCTTCCAGCGCTACCTGGGCATCTGCCACCCC    420
 111 GlySerIleLeuPheLeuThrCysIleSerPheGlnArgTyrLeuGlyIleCysHisPro    131

 421 CTGGCTTCCTGGCACAAGCGTGGAGGTCGCCGTGCTGCTTGGGTAGTGTGTGGAGTCGTG    480
 131 LeuAlaSerTrpHisLysArgGlyGlyArgArgAlaAlaTrpValValCysGlyValVal    151

 481 TGGCTGGCTGTGACAGCCCAGTGCCTGCCCACGGCAGTCTTTGCTGCCACAGGCATCCAG    540
 151 TrpLeuAlaValThrAlaGlnCysLeuProThrAlaValPheAlaAlaThrGlyIleGln    171

 541 CGCAACCGCACTGTGTGCTACGACCTGAGCCCACCCATCCTGTCTACTCGCTACCTGCCC    600
 171 ArgAsnArgThrValCysTyrAspLeuSerProProIleLeuSerThrArgTyrLeuPro    191

 601 TATGGTATGGCCCTCACGGTCATCGGCTTCTTGCTGCCCTTCATAGCCTTACTGGCTTGT    660
 191 TyrGlyMetAlaLeuThrValIleGlyPheLeuLeuProPheIleAlaLeuLeuAlaCys    211

 661 TATTGTCGCATGGCCCGCCGCCTGTGTCGCCAGGATGGCCCAGCAGGTCCTGTGGCCCAA    720
 211 TyrCysArgMetAlaArgArgLeuCysArgGlnAspGlyProAlaGlyProValAlaGln    231

 721 GAGCGGCGCAGCAAGGCGGCTCGTATGGCTGTGGTGGTGGCAGCTGTCTTTGCCATCAGC    780
 231 GluArgArgSerLysAlaAlaArgMetAlaValValValAlaAlaValPheAlaIleSer    251

 781 TTCCTGCCTTTCCACATCACCAAGACAGCCTACTTGGCTGTGCGCTCCACGCCCGGTGTC    840
 251 PheLeuProPheHisIleThrLysThrAlaTyrLeuAlaValArgSerThrProGlyVal    271

 841 TCTTGCCCTGTGCTGGAGACCTTCGCTGCTGCCTACAAAGGCACTCGGCCCTTCGCCAGT    900
 271 SerCysProValLeuGluThrPheAlaAlaAlaTyrLysGlyThrArgProPheAlaSer    291

 901 GTCAACAGTGTTCTGGACCCCATTCTCTTCTACTTCACACAACAGAAGTTCCGGCGGCAA    960
 291 ValAsnSerValLeuAspProIleLeuPheTyrPheThrGlnGlnLysPheArgArgGln    311

 961 CCCCACGATCTCTTACAGAGGCTCACAGCCAAGTGGCAGAGGCAGAGAGTCTGAGGCCCC   1020
 311 ProHisAspLeuLeuGlnArgLeuThrAlaLysTrpGlnArgGlnArgVal***          329
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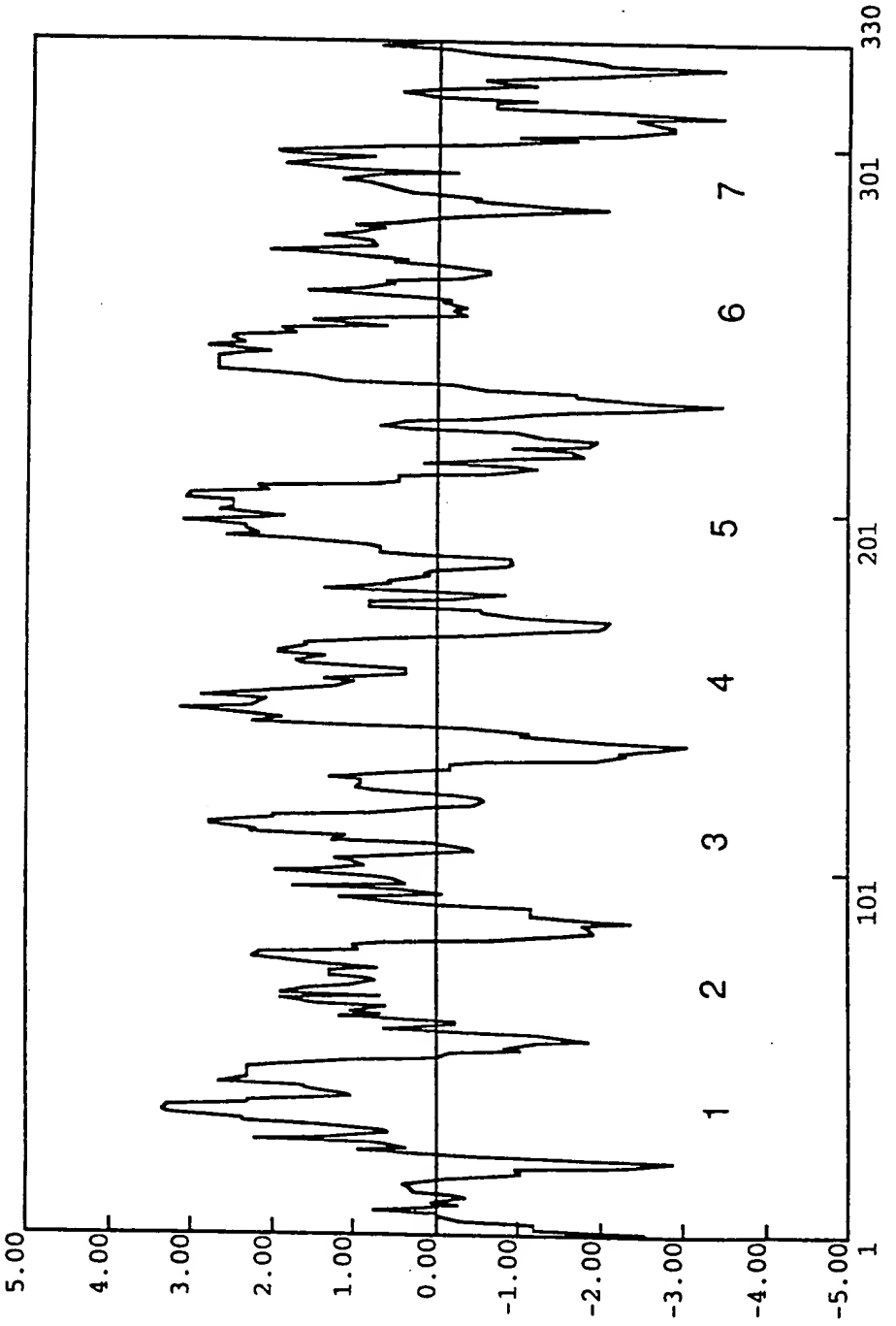


FIGURE 70

FIGURE 71

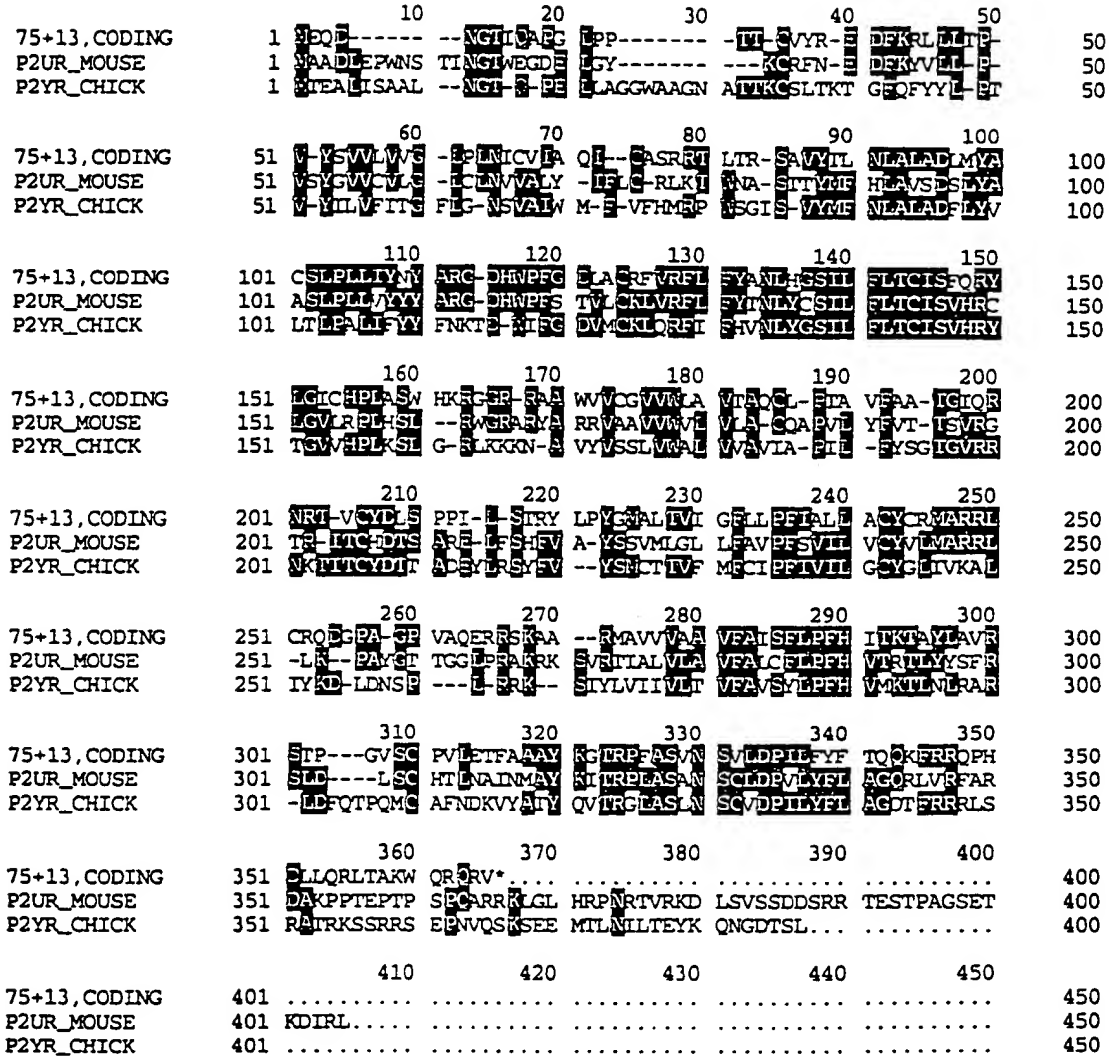


FIGURE 72

```
             9          18          27          36          45          54
5' GCC ACC AAC GTG TTC ATC CTG TCA CTG GCC GAT GTG CTG GTG ACA GCC ATC TGC
                                       --- --- --- --- --- --- --- --- ---
                                       Ala Asp Val Leu Val Thr Ala Ile Cys

            63          72          81          90          99         108
   CTG CCG GCC AGT CTG CTG GTA GAC ATC ACG GAA TCC TGG CTC TTT GGC CAT GCC
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Leu Pro Ala Ser Leu Leu Val Asp Ile Thr Glu Ser Trp Leu Phe Gly His Ala

           117         126         135         144         153         162
   CTC TGC AAG GTC ATC CCC TAT CTA CAG GCC GTG TCC GTG TCA GTG GTC GTG CTG
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Leu Cys Lys Val Ile Pro Tyr Leu Gln Ala Val Ser Val Ser Val Val Val Leu

           171         180         189         198         207         216
   ACT CTC AGC TCC ATC GCC CTG GAC CGC TGG TAC GCC ATC TGC CAC CCG CTG TTG
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Thr Leu Ser Ser Ile Ala Leu Asp Arg Trp Tyr Ala Ile Cys His Pro Leu Leu

           225         234         243         252         261         270
   TTC AAG AGC ACT GCC CGG CGC GCC CGC GGC TCC ATC CTC GGC ATC TGG GCG GTG
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Phe Lys Ser Thr Ala Arg Arg Ala Arg Gly Ser Ile Leu Gly Ile Trp Ala Val

           279         288         297         306         315         324
   TCG CTG GCT GTC ATG GTG CCT CAG GCT GCT GTC ATG GAG TGT AGC AGC GTG CTG
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Ser Leu Ala Val Met Val Pro Gln Ala Ala Val Met Glu Cys Ser Ser Val Leu

           333         342         351         360         369         378
   CCC GAG CTG GCC AAC CGC ACC CGC CTC CTG TCT GTC TGT GAT GAG CGC TGG GCA
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Pro Glu Leu Ala Asn Arg Thr Arg Leu Leu Ser Val Cys Asp Glu Arg Trp Ala

           387         396         405         414         423         432
   GAC GAC CTG TAC CCC AAG ATC TAC CAC AGC TGC TTC TTC ATT GTC ACC TAC CTG
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Asp Asp Leu Tyr Pro Lys Ile Tyr His Ser Cys Phe Phe Ile Val Thr Tyr Leu

           441         450         459         468         477         486
   GCC CCA CTG GGC CTC ATG GCC ATG GCC TAT TTC CAG ATC TTC CGC AAG CTC TGG
   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   Ala Pro Leu Gly Leu Met Ala Met Ala Tyr Phe Gln Ile Phe Arg Lys Leu Trp

           495         504         513         522         531         540
   GGC CGC CAG ATC CCC GGC ACC ACC TCG GCC CTG GTG CGC AAC TGG AAG CGG CCC
```

FIGURE 73

```
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Gly Arg Gln Ile Pro Gly Thr Thr Ser Ala Leu Val Arg Asn Trp Lys Arg Pro

        549         558         567         576         585         594
TCA GAC CAG CTG GAC GAC CAG GGC CAG GGC CTG AGC TCA GAG CCC CAG CCC CGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Ser Asp Gln Leu Asp Asp Gln Gly Gln Gly Leu Ser Ser Glu Pro Gln Pro Arg

        603         612         621         630         639         648
GCC CGC GCC TTC CTG GCC GAG GTG AAA CAG ATG CGA GCC CGG AGG AAG ACG GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Ala Arg Ala Phe Leu Ala Glu Val Lys Gln Met Arg Ala Arg Arg Lys Thr Ala

        657         666         675         684         693         702
AAG ATG CTG ATG GTG GTG CTG CTG GTC TTC GCC CTC TGC TAC CTG CCC ATC AGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Lys Met Leu Met Val Val Leu Leu Val Phe Ala Leu Cys Tyr Leu Pro Ile Ser

        711         720         729         738         747         756
GTC CTC AAC GTC CTC AAG AGG GTC TTC GGG ATG TTC CGC CAA GCC AGC GAC CGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Val Leu Asn Val Leu Lys Arg Val Phe Gly Met Phe Arg Gln Ala Ser Asp Arg

        765         774         783         792         801         810
GAG GCC ATC TAC GCC TGC TTC ACC TTC TCC CAC TGG CTG GTG TAC GCC AAC AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Glu Ala Ile Tyr Ala Cys Phe Thr Phe Ser His Trp Leu Val Tyr Ala Asn Ser

        819         828         837
GCC GCC AAT CCC CTC CTC TAC TCC TTC CTC CCT 3'
--- ---
Ala Ala
```

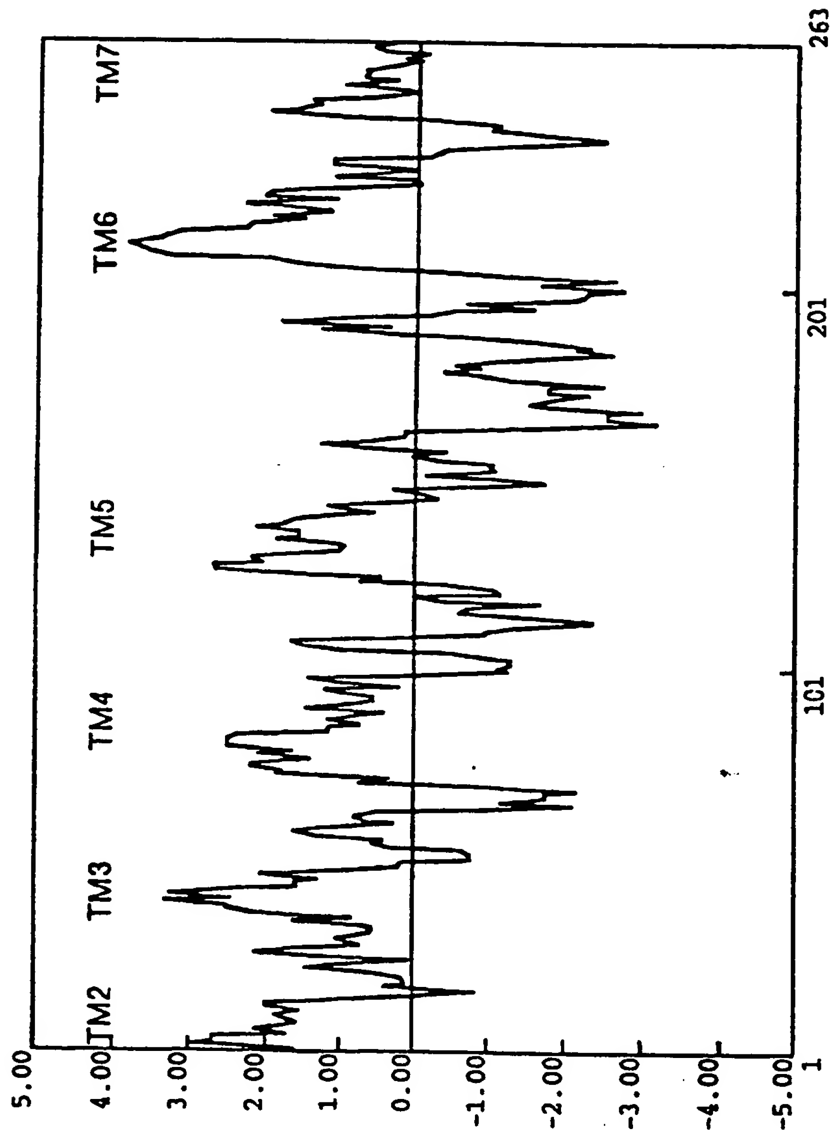

TM2
TM3
TM4
TM5
TM6
TM7
5.00
4.00
3.00
2.00
1.00
0.00
-1.00
-2.00
-3.00
-4.00
-5.00
1
101
201
263

FIGURE 74

FIGURE 75

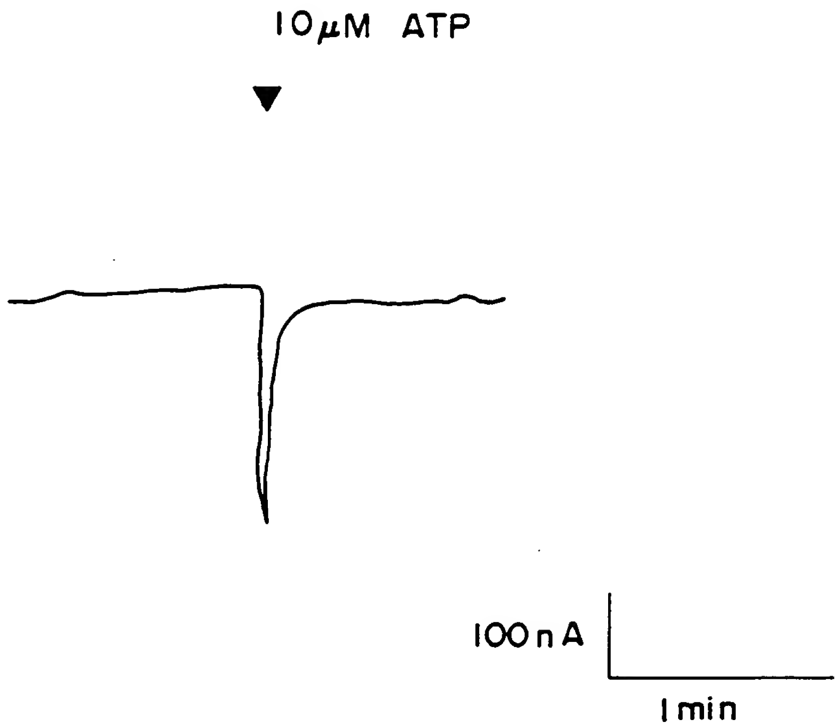


FIGURE 76

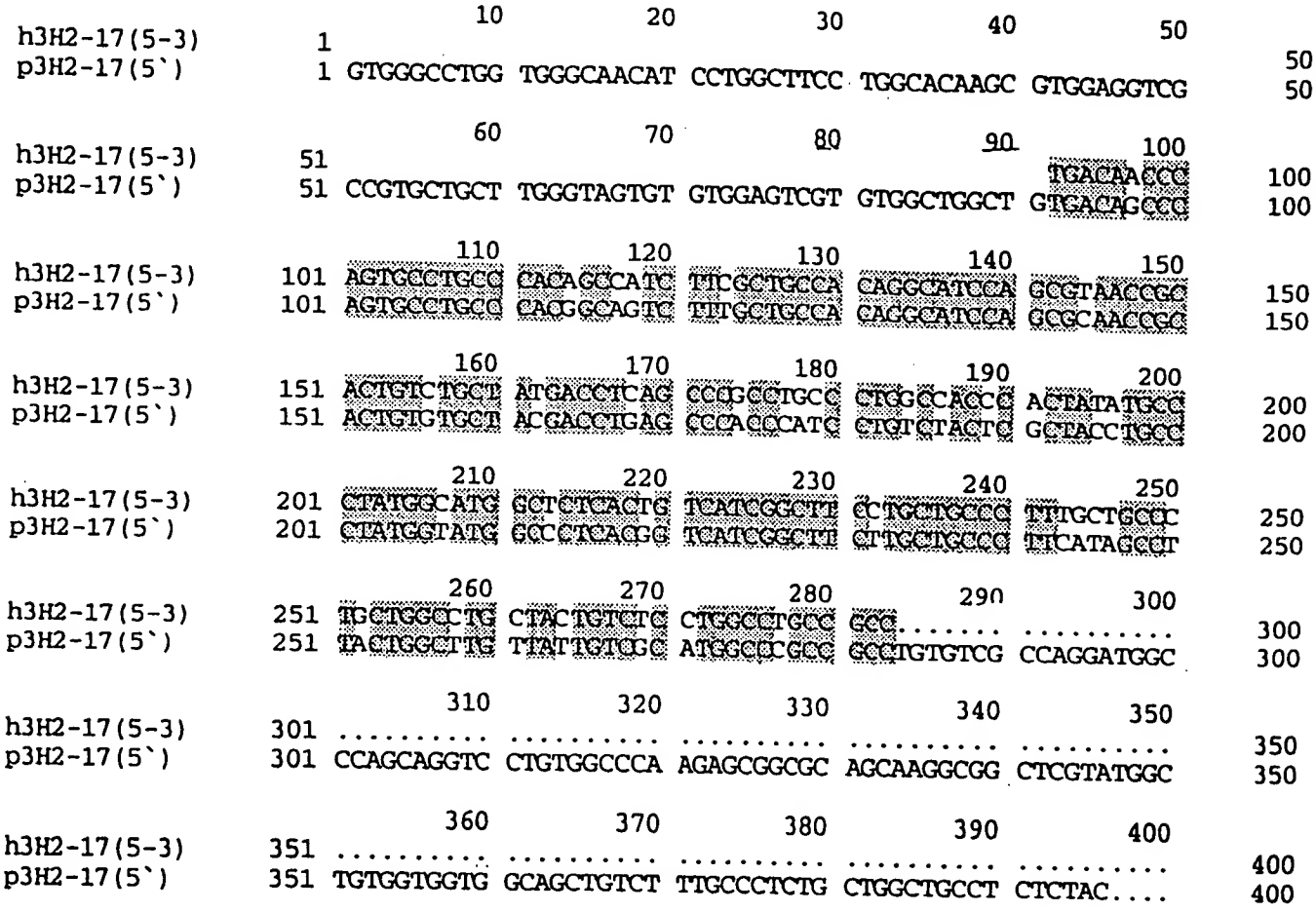

h3H2-17(5-3)
p3H2-17(5`)
10 20 30 40 50
1 GTGGGCCTGG TGGGCAACAT CCTGGCTTCC TGGCACAAGC GTGGAGGTCG 50
1 GTGGGCCTGG TGGGCAACAT CCTGGCTTCC TGGCACAAGC GTGGAGGTCG 50
60 70 80 90 100
51 CCGTGCTGCT TGGGTAGTGT GTGGAGTCGT GTGGCTGGCT GTGACAACCC 100
51 CCGTGCTGCT TGGGTAGTGT GTGGAGTCGT GTGGCTGGCT GTGACAGCCC 100
110 120 130 140 150
101 AGTGCCTGCC CACAGCCATC TTCGCTGCCA CAGGCATCCA GCGTAACCGC 150
101 AGTGCCTGCC CACGGCAGTC TTTGCTGCCA CAGGCATCCA GCGCAACCGC 150
160 170 180 190 200
151 ACTGTCTGCT ATGACCTCAG CCGGCCTGCC CTGGCCACCC ACTATATGCC 200
151 ACTGTGTGCT ACGACCTGAG CCCACCCATC CTGTCTACTC GCTACCTGCC 200
210 220 230 240 250
201 CTATGGCATG GCTCTCACTG TCATCGGCTT CCTGCTGCCC TTTGCTGCTC 250
201 CTATGGTATG GCCCTCACGG TCATCGGCTT CTTGCTGCCC TTCATAGCCT 250
260 270 280 290 300
251 TGCTGGCCTG CTACTGTCTC CTGGCCTGCC GCC..... 300
251 TACTGGCTTG TTATTGTCGC ATGGCCGCCC GCCTGTGTCG CCAGGATGGC 300
310 320 330 340 350
301 350
301 CCAGCAGGTC CTGTGGCCCA AGAGCGGCGC AGCAAGGCGG CTCGTATGGC 350
360 370 380 390 400
351 400
351 TGTGGTGGTG GCAGCTGTCT TTGCCCTCTG CTGGCTGCCT CTCTAC.... 400

FIGURE 77

```
   1 TGACTCCCTGAACATAGGAAACCCACCTGGGCAGCCATGGAATGGGACAATGGCACAGGC   60
   1                                  MetGluTrpAspAsnGlyThrGly      8

  61 CAGGCTCTGGGCTTGCCACCCACCACCTGTGTCTACCGCGAGAACTTCAAGCAACTGCTG  120
   8 GlnAlaLeuGlyLeuProProThrThrCysValTyrArgGluAsnPheLysGlnLeuLeu   28

 121 CTGCCACCTGTGTATTCGGCGGTGCTGGCGGCTGGCCTGCCGCTGAACATCTGTGTCATT  180
  28 LeuProProValTyrSerAlaValLeuAlaAlaGlyLeuProLeuAsnIleCysValIle   48

 181 ACCCAGATCTGCACGTCCCGCCGGGCCCTGACCCGCACGGCCGTGTACACCCTAAACCTT  240
  48 ThrGlnIleCysThrSerArgArgAlaLeuThrArgThrAlaValTyrThrLeuAsnLeu   68

 241 GCTCTGGCTGACCTGCTATATGCCTGCTCCCTGCCCCTGCTCATCTACAACTATGCCCAA  300
  68 AlaLeuAlaAspLeuLeuTyrAlaCysSerLeuProLeuLeuIleTyrAsnTyrAlaGln   88

 301 GGTGATCACTGGCCCTTTGGCGACTTCGCCTGCCGCCTGGTCCGCTTCCTCTTCTATGCC  360
  88 GlyAspHisTrpProPheGlyAspPheAlaCysArgLeuValArgPheLeuPheTyrAla  108

 361 AACCTGCACGGCAGCATCCTCTTCCTCACCTGCATCAGCTTCCAGCGCTACCTGGGCATC  420
 108 AsnLeuHisGlySerIleLeuPheLeuThrCysIleSerPheGlnArgTyrLeuGlyIle  128

 421 TGCCACCCGCTGGCCCCCTGGCACAAACGTGGGGGCCGCCGGGCTGCCTGGCTAGTGTGT  480
 128 CysHisProLeuAlaProTrpHisLysArgGlyGlyArgArgAlaAlaTrpLeuValCys  148

 481 GTAACCGTGTGGCTGGCCGTGACAACCCAGTGCCTGCCCACAGCCATCTTCGCTGCCACA  540
 148 ValThrValTrpLeuAlaValThrThrGlnCysLeuProThrAlaIlePheAlaAlaThr  168

 541 GGCATCCAGCGTAACCGCACTGTCTGCTATGACCTCAGCCCGCCTGCCCTGGCCACCCAC  600
 168 GlyIleGlnArgAsnArgThrValCysTyrAspLeuSerProProAlaLeuAlaThrHis  188

 601 TATATGCCCTATGGCATGGCTCTCACTGTCATCGGCTTCCTGCTGCCCTTTGCTGCCCTG  660
 188 TyrMetProTyrGlyMetAlaLeuThrValIleGlyPheLeuLeuProPheAlaAlaLeu  208

 661 CTGGCCTGCTACTGTCTCCTGGCCTGCCGCCTGTGCCGCCAGGATGGCCCGGCAGAGCCT  720
 208 LeuAlaCysTyrCysLeuLeuAlaCysArgLeuCysArgGlnAspGlyProAlaGluPro  228

 721 GTGGCCCAGGAGCGGCGTGGCAAGGCGGCCCGCATGGCCGTGGTGGTGGCTGCTGCCTTT  780
 228 ValAlaGlnGluArgArgGlyLysAlaAlaArgMetAlaValValValAlaAlaAlaPhe  248

 781 GCCATCAGCTTCCTGCCTTTTCACATCACCAAGACAGCCTACCTGGCAGTGGGCTCGACG  840
 248 AlaIleSerPheLeuProPheHisIleThrLysThrAlaTyrLeuAlaValGlySerThr  268

 841 CCGGGCGTCCCCTGCACTGTATTGGAGGCCTTTGCAGCGGCCTACAAAGGCACGCGGCCG  900
 268 ProGlyValProCysThrValLeuGluAlaPheAlaAlaAlaTyrLysGlyThrArgPro  288

 901 TTTGCCAGTGCCAACAGCGTGCTGGACCCCATCCTCTTCTACTTCACCCAGAAGAAGTTC  960
 288 PheAlaSerAlaAsnSerValLeuAspProIleLeuPheTyrPheThrGlnLysLysPhe  308

 961 CGCCGGCGACCACATGAGCTCCTACAGAAACTCACAGCCAAATGGCAGAGGCAGGGTCGC 1020
 308 ArgArgArgProHisGluLeuLeuGlnLysLeuThrAlaLysTrpGlnArgGlnGlyArg  328

1021 TGA                                                          1023
 328 ***                                                           329
```

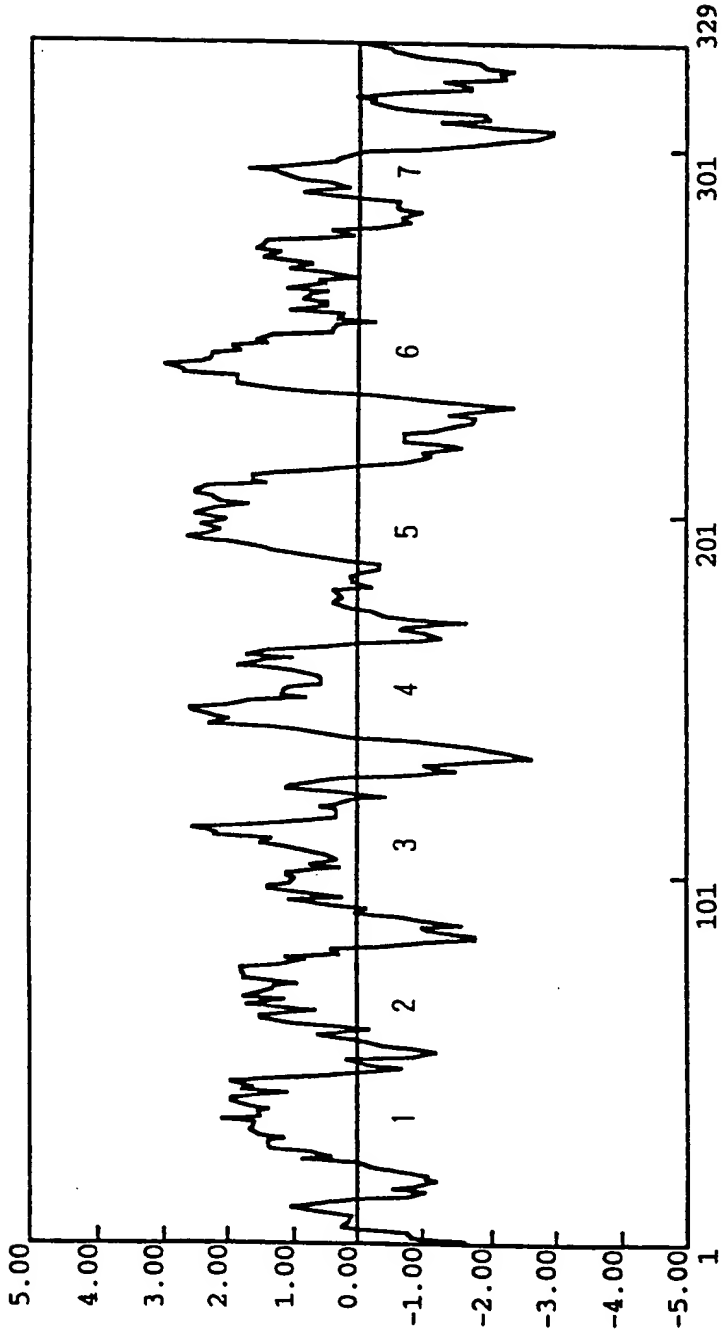
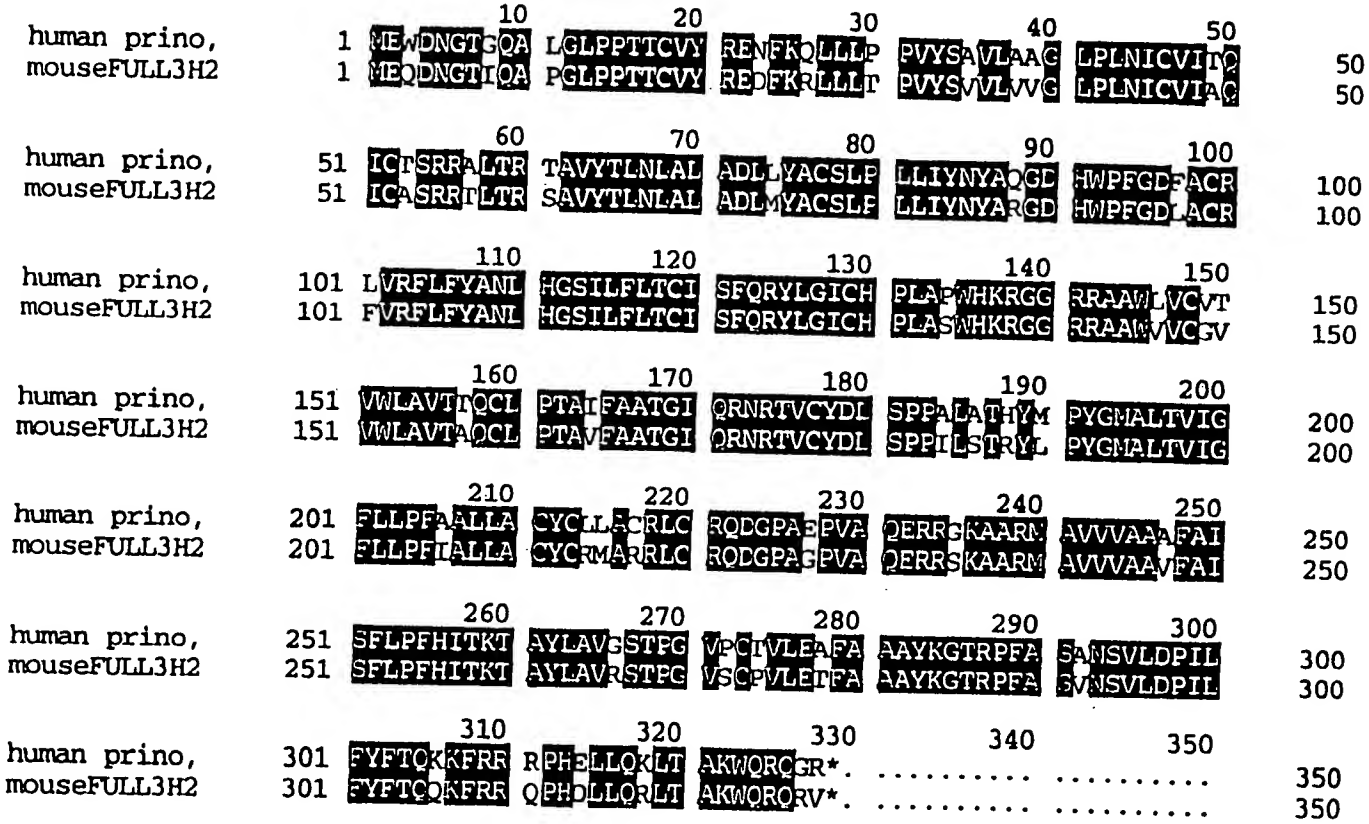


FIGURE 78

FIGURE 79


human prino,
mouseFULL3H2
human prino,
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human prino,
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human prino,
mouseFULL3H2
human prino,
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